



QY 421 CTGTCAATAGCAAGTGTGATGTAATGTCGGCGGTCAATGTTAGATATGCAAGC 480  
| | | | |  
Db 421 CTGTCAATAGCAAGTGTGATGTAATGTCGGCGGTCAATGTTAGATATGCAAGC 480  
QY 481 GAAGGCCAACCAATTGATCTTGAACCTTGGAAAATGATACAAAACAAAACAGAGCA 540  
| | | | |  
Db 481 GAAGGCCAACCAATTGATCTTGAACCTTGGAAAATGATACAAAACAAAACAGAGCA 540  
QY 541 TTATTAACTTTGGCGTTATAGTCAGCAGATATCGCTAATGTCGATGATCAACTTAA 600  
| | | | |  
Db 541 TTATTAACTTTGGCGTTATAGTCAGCAGATATCGCTAATGTCGATGATCAACTTAA 600  
QY 601 GAACATTTAGAAAGTTATAGTATCATTTAGTATGATGTCAGATTAAGATGATTTA 660  
| | | | |  
Db 601 GAACATTTAGAAAGTTATAGTATCATTTAGTATGATGTCAGATTAAGATGATTTA 660  
QY 661 TTAGACTGCTATGCTGATGAAAGCAAGTTAGTAAAAAAGTGGCAGCGATCTTGAAT 720  
| | | | |  
Db 661 TTAGACTGCTATGCTGATGAAAGCAAGTTAGTAAAAAAGTGGCAGCGATCTTGAAT 720  
QY 721 AATTAAGTACGTACGTGAGTTTATAGGAAAAGATGCGCAGAAATTAATGACTTAT 780  
| | | | |  
Db 721 AATTAAGTACGTACGTGAGTTTATAGGAAAAGATGCGCAGAAATTAATGACTTAT 780  
QY 781 CATAGAGACGACGATGATGAACTAACCAATTGATGAAATCAATACAAAACAC 840  
| | | | |  
Db 781 CATAGAGACGACGATGATGAACTAACCAATTGATGAAATCAATACAAAACAC 840  
QY 841 TTATTAGAAATCGTTGATTTA 861  
| | | | |  
Db 841 TTATTAGAAATCGTTGATTTA 861

RESULT 2  
US-09-134-001C-334  
; Sequence 334, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 334  
; LENGTH: 909  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-334

Query Match 2.9%; Score 25; DB 4; Length 909;  
Best Local Similarity 100.0%; Pred. No. 0.0051;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAGGAAATTAACAATCATTAAGT 305  
| | | | |  
Db 308 GAGGAAATTAACAATCATTAAGT 332

RESULT 3  
US-09-484-970B-110  
; Sequence 110, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmuth, Wayne  
; APPLICANT: Walker, Michael G.

; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 110  
; LENGTH: 763  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 009051.5CB1  
US-09-484-970B-110

Query Match 2.1%; Score 18; DB 4; Length 763;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GATGAATTAATTATAGA 32  
| | | | |  
Db 212 GATGAATTAATTATAGA 229

RESULT 4  
US-07-686-322A-1  
; Sequence 1, Application US/07686322A  
; Patent No. 5312733  
; GENERAL INFORMATION:  
; APPLICANT: MacLeod Dr., Carol L.  
; TITLE OF INVENTION: No. 5312733el T-cell lymphoma cDNA clones  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
ADDRESSER: Patent Department, Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/686,322A  
CLASSIFICATION: 435  
FILING DATE: 19910411  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/509684  
FILING DATE: 13-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauener, Charlene A.  
REGISTRATION NUMBER: 33,035  
REFERENCE/DOCKET NUMBER: D-5232-CIP  
TELEPHONE: (713) 651-3634  
TELEFAX: (713) 651-5246  
TELEX: Western Union 762829  
; INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1301 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: AKR1 Jackson  
INDIVIDUAL ISOLATE: SL12 cell line  
TISSUE TYPE: Lymphoma  
CELL TYPE: T-cell  
CELL LINE: SL12.3 and SL12.4

IMMEDIATE SOURCE:  
CLONE: 19.1  
US-07-686-322A-1

Query Match 2.1%; Score 18; DB 1; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CAATACAAAACCTTATT 845  
DB 3 CAATACAAAACCTTATT 20

RESULT 5

US-08-002-999-1  
Sequence 1, Application US/08002999  
Patent No. 5440017  
GENERAL INFORMATION:  
APPLICANT: Macleod Dr., Carol L.  
TITLE OF INVENTION: No. 5440017el T-cell lymphoma cDNA clones  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patent Department, Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/002,999  
FILING DATE: 19930111  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/686,322  
FILING DATE: 11-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Benjamin A.  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D-532-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 651-5587  
TELEFAX: (713) 651-5246  
TELEX: Western Union 762829  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1301 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Mouse  
STRAIN: AKR1 Jackson  
INDIVIDUAL ISOLATE: SUI2 cell line  
TISSUE TYPE: Lymphoma  
CELL TYPE: T-cell  
CELL LINE: SUI2.3 and SUI2.4  
IMMEDIATE SOURCE:  
CLONE: 19.1  
US-08-002-999-1

Query Match 2.1%; Score 18; DB 1; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CAATACAAAACCTTATT 845  
DB 3 CAATACAAAACCTTATT 20

RESULT 6  
US-08-700-651-1  
Sequence 1, Application US/08700651B  
Patent No. 6015882  
GENERAL INFORMATION:  
APPLICANT: PETERSEN, CAROLYN  
APPLICANT: LEECH, JAMES  
APPLICANT: NELSON, RICHARD, C.  
APPLICANT: GUT, JIRI  
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs  
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum  
FILE REFERENCE: 480.19-4(HV)  
CURRENT APPLICATION NUMBER: US/08/700,651B  
CURRENT FILING DATE: 1997-08-14  
EARLIER APPLICATION NUMBER: 08/415,751  
EARLIER FILING DATE: 1995-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 5163  
TYPE: DNA  
ORGANISM: Cryptosporidium parvum  
US-08-700-651-1

Query Match 2.1%; Score 18; DB 3; Length 5163;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCATGATCTTGAACCT 507  
DB 3769 CCATGATCTTGAACCT 3786

RESULT 7

US-08-928-361B-4  
Sequence 4, Application US/08928361B  
Patent No. 6071518  
GENERAL INFORMATION:  
APPLICANT: Petersen, Carolyn  
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,  
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS  
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PETERS, VERNY, JONES & BIKSA  
STREET: 385 Sherman Avenue, Suite 6  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306-1840  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,361B  
FILING DATE: 12-SEP-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,062  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: VERNY, Hana  
REGISTRATION NUMBER: 30,518  
REFERENCE/DOCKET NUMBER: 480.76-1(HV)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-1677  
TELEFAX: 650-324-1678

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5163 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-928-361B-4

Query Match 2.1%; Score 18; DB 3; Length 5163;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507  
DB 3769 CCAATTGATCTTGAACACT 3786

## RESULT 8

US-09-588-995A-4  
Sequence 4, Application US/09588995A  
Patent No. 6514697  
GENERAL INFORMATION:  
APPLICANT: PETERSEN, CAROLYN  
APPLICANT: BARNES, DEBRA A.  
APPLICANT: NELSON, RICHARD C.  
APPLICANT: GUT, JIRI  
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND  
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM  
FILE REFERENCE: 480.19-5  
CURRENT APPLICATION NUMBER: US/09/588,995A  
CURRENT FILING DATE: 2000-06-06  
PRIOR APPLICATION NUMBER: 08/827,171  
PRIOR FILING DATE: 1997-03-27  
PRIOR APPLICATION NUMBER: 08/928,361  
PRIOR FILING DATE: 1997-09-12  
PRIOR APPLICATION NUMBER: 08/700,651  
PRIOR FILING DATE: 1996-08-14  
PRIOR APPLICATION NUMBER: 08/415,751  
PRIOR FILING DATE: 1995-04-03  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 4  
LENGTH: 5163  
TYPE: DNA  
ORGANISM: Cryptosporidium parvum  
US-09-588-995A-4

Query Match 2.1%; Score 18; DB 4; Length 5163;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507  
DB 3769 CCAATTGATCTTGAACACT 3786

## RESULT 9

US-08-700-651-2  
Sequence 2, Application US/08700651B  
Patent No. 6015882  
GENERAL INFORMATION:  
APPLICANT: PETERSEN, CAROLYN  
APPLICANT: LEECH, JAMES  
APPLICANT: NELSON, RICHARD, C.  
APPLICANT: GUT, JIRI  
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs  
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum  
FILE REFERENCE: 480.19-4 (HV)  
CURRENT APPLICATION NUMBER: US/08/700,651B  
CURRENT FILING DATE: 1997-08-14

EARLIER APPLICATION NUMBER: 08/415,751  
EARLIER FILING DATE: 1995-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 5318  
TYPE: DNA  
ORGANISM: Cryptosporidium parvum  
US-08-700-651-2

Query Match 2.1%; Score 18; DB 3; Length 5318;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507  
DB 3769 CCAATTGATCTTGAACACT 3786

## RESULT 10

US-08-928-361B-3  
Sequence 3, Application US/08928361B  
Patent No. 6071518  
GENERAL INFORMATION:  
APPLICANT: Petersen, Carolyn  
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,  
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS  
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PETERS, VERNY, JONES & BIKSA  
STREET: 385 Sherman Avenue, Suite 6  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306-1840  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,361B  
FILING DATE: 12-SEP-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,062  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verny, Hana  
REGISTRATION NUMBER: 30,518  
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-1677  
TELEFAX: 650-324-1678  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5318 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-928-361B-3

Query Match 2.1%; Score 18; DB 3; Length 5318;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507  
DB 3769 CCAATTGATCTTGAACACT 3786



## RESULT 11

US-09-588-995A-3  
Sequence 3, Application US/09588995A  
Patent No. 6514697  
GENERAL INFORMATION:  
APPLICANT: PETERSEN, CAROLYN  
APPLICANT: BARNES, DEBRA A.  
APPLICANT: NELSON, RICHARD C.  
APPLICANT: GUT, JIRI  
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND  
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM  
FILE REFERENCE: 480.19-5  
CURRENT APPLICATION NUMBER: US/09/588,995A  
CURRENT FILING DATE: 2000-06-06  
PRIOR APPLICATION NUMBER: 08/827,171  
PRIOR FILING DATE: 1997-03-27  
PRIOR APPLICATION NUMBER: 08/928,361  
PRIOR FILING DATE: 1997-09-12  
PRIOR APPLICATION NUMBER: 08/700,651  
PRIOR FILING DATE: 1996-08-14  
PRIOR APPLICATION NUMBER: 08/415,751  
PRIOR FILING DATE: 1995-04-03  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 5318  
TYPE: DNA  
ORGANISM: Cryptosporidium parvum  
US-09-588-995A-3

Query Match 2.1%; Score 18; DB 4; Length 5318;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCATGATCTTGAAGT 507  
DB 3769 CCATGATCTTGAAGT 3786

RESULT 12  
US-09-702-705-1416  
Sequence 1416, Application US/09702705  
Patent No. 6504010  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C14  
CURRENT APPLICATION NUMBER: US/09/702,705  
CURRENT FILING DATE: 2000-10-30  
NUMBER OF SEQ ID NOS: 1833  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1416  
LENGTH: 540  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-702-705-1416

Query Match 2.0%; Score 17; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 AAGTAAATTAAGTT 411

DB 522 AAGTAAATTAAGTT 538

RESULT 13  
US-09-736-457-1416  
Sequence 1416, Application US/09736457  
Patent No. 6509448  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C15  
CURRENT APPLICATION NUMBER: US/09/736,457  
CURRENT FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 1864  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1416  
LENGTH: 540  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-736-457-1416

Query Match 2.0%; Score 17; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 AAGTAAATTAAGTT 411  
DB 522 AAGTAAATTAAGTT 538

RESULT 14  
US-09-385-982-404  
Sequence 404, Application US/09385982  
Patent No. 6262334  
GENERAL INFORMATION:  
APPLICANT: ENDEGE, WILSON O., ET AL.  
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
TITLE OF INVENTION: PRODUCTS: II  
FILE REFERENCE: CCDNA-260XX  
CURRENT APPLICATION NUMBER: US/09/385,982  
CURRENT FILING DATE: 1999-08-30  
EARLIER APPLICATION NUMBER: 09/328,111  
EARLIER FILING DATE: 1999-06-08  
EARLIER APPLICATION NUMBER: 60/117,393  
EARLIER FILING DATE: 1999-01-27  
EARLIER APPLICATION NUMBER: 60/098,639  
EARLIER FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 544  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 404  
LENGTH: 604  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(604)  
OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-404

Query Match 2.0%; Score 17; DB 3; Length 604;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 CTCAGCTAGAAGAACT 99  
 Db 289 CTCAGCTAGAAGAACT 305

RESULT 15

US-09-385-982-173  
 ; Sequence 173, Application US/09385982  
 ; Patent No. 6262334  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ENDEGE, WILSON O., ET AL.  
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
 ; FILE REFERENCE: CCDNA-260XX  
 ; CURRENT APPLICATION NUMBER: US/09/385,982  
 ; EARLIER FILING DATE: 1999-06-30  
 ; EARLIER APPLICATION NUMBER: 09/328,111  
 ; EARLIER FILING DATE: 1999-06-08  
 ; EARLIER APPLICATION NUMBER: 60/117,393  
 ; EARLIER FILING DATE: 1999-01-27  
 ; EARLIER APPLICATION NUMBER: 60/098,639  
 ; EARLIER FILING DATE: 1998-08-31  
 ; NUMBER OF SEQ ID NOS: 544  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 173  
 ; LENGTH: 616  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(616)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-385-982-173

Query Match 2.0%; Score 17; DB 3; Length 616;  
 Best Local Similarity 100.0%; Pred.No. 50;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 CTCAGCTAGAAGAACT 99  
 Db 286 CTCAGCTAGAAGAACT 302

Search completed: November 29, 2003, 17:03:58  
 Job time : 76 secs

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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 16:19:20 ; Search time 336 Seconds

(without alignments)  
8442.643 Million cell updates/sec

Title: US-09-925-637-63

Perfect score: 861  
Sequence: 1 atgacgaactacacgatgaa.....tattagaactcgttgattta 861

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Gapop 60.0 , Gapext 60.0

Searched: 2190069 seqs, 1647345023 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	861	100.0	861	10	US-09-925-637-63 Sequence 63, Appl
2	861	100.0	861	14	US-10-084-205-63 Sequence 155, App
3	861	100.0	1893	8	US-08-781-986A-155 Sequence 8485, Ap
4	489	56.8	882	9	US-09-815-242-8485 Sequence 4184, Ap
5	474	55.1	864	9	US-09-815-242-4184 Sequence 2822, Ap
6	413	48.0	413	9	US-09-815-242-2822 Sequence 3275, Ap
7	337	39.1	337	9	US-09-815-242-3275 Sequence 24950, A
8	19	2.2	151	9	US-09-864-761-24950 Sequence 194294, A
9	19	2.2	580	12	US-10-027-632-194294 Sequence 194295, A
10	19	2.2	580	13	US-10-027-632-194295 Sequence 194296, A
11	19	2.2	580	13	US-10-027-632-194296 Sequence 194297, A
12	19	2.2	580	13	US-10-027-632-194297 Sequence 8212, Ap
13	19	2.2	922	12	US-10-027-632-21738 Sequence 21738, A
14	19	2.2	922	12	US-10-027-632-21738 Sequence 21739, A
15	19	2.2	922	12	US-10-027-632-21739 Sequence 21738, A
16	19	2.2	922	13	US-10-027-632-21738 Sequence 21738, A

17	19	2.2	922	13	US-10-027-632-21739	Sequence 21739, A
18	19	2.2	130427	14	US-10-175-523-87	Sequence 87, Appl
19	19	2.2	640681	10	US-09-790-988-1	Sequence 1, Appl
20	19	2.2	2940817	12	US-10-027-632-174763	Sequence 174763, Appl
21	19	2.2	2940917	13	US-10-027-632-174763	Sequence 174763, Appl
22	18	2.1	118	9	US-09-764-878-357	Sequence 357, App
23	18	2.1	118	14	US-10-079-854-357	Sequence 357, App
24	18	2.1	322	13	US-10-040-733-374	Sequence 374, App
25	18	2.1	449	10	US-09-983-965-3145	Sequence 3145, Ap
26	18	2.1	509	12	US-10-027-632-26964	Sequence 26964, A
27	18	2.1	509	13	US-10-027-632-26964	Sequence 26964, A
28	18	2.1	562	12	US-10-027-632-114822	Sequence 114822, A
29	18	2.1	562	13	US-10-027-632-114822	Sequence 114822, A
30	18	2.1	637	12	US-10-027-632-189412	Sequence 189412, A
31	18	2.1	637	12	US-10-027-632-189412	Sequence 189412, A
32	18	2.1	637	13	US-10-027-632-189412	Sequence 189412, A
33	18	2.1	637	13	US-10-027-632-189413	Sequence 189413, A
34	18	2.1	721	10	US-09-764-868-109	Sequence 1, Appl
35	18	2.1	1048	12	US-10-097-896-1	Sequence 257935, A
36	18	2.1	1154	12	US-10-027-632-257935	Sequence 257935, A
37	18	2.1	1154	13	US-10-027-632-257935	Sequence 257935, A
38	18	2.1	1408	11	US-09-822-846-54	Sequence 54, Appl
39	18	2.1	2064	11	US-09-822-846-55	Sequence 55, Appl
40	18	2.1	6638	9	US-09-764-869-1645	Sequence 1645, Ap
41	18	2.1	2064	11	US-10-091-504-1645	Sequence 1645, Ap
42	18	2.1	10146	8	US-08-781-986A-243	Sequence 243, App
43	18	2.1	42663	12	US-10-017-161-1017	Sequence 1017, Ap
44	18	2.1	99014	10	US-09-880-107-3428	Sequence 3428, Ap
45	18	2.1	175590	11	US-09-911-077A-13	Sequence 13, Appl

## ALIGNMENTS

RESULT 1  
US-09-925-637-63  
; Sequence 63, Application US/09925637  
; Patent No. US2002010338A1  
; GENERAL INFORMATION:  
; APPLICANT: CRO1  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
; FILE REFERENCE: PB560  
; CURRENT APPLICATION NUMBER: US/09/925,637  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/23773  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 60/151,933  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: US 08/781,986  
; PRIOR FILING DATE: 1997-01-03  
; PRIOR APPLICATION NUMBER: US 08/956,171  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/009,861  
; PRIOR FILING DATE: 1996-01-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 861  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-637-63  
Query Match 100.0%; Score 861; DB 10; Length 861;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGAACCTACCGATGATATTAATGATGAGTAAATTAATGATGCTTGGC 60  
DB 1 ATGACGAACCTACCGATGATATTAATGATGAGTAAATTAATGATGCTTGGC 60  
QY 61 ATTAATTAATCGTATGATGATCTAGCTAGAGAAAGATGATGATTCATTAAATGCT 120  
DB 61 ATTAATTAATCGTATGATGATCTAGCTAGAGAAAGATGATGATTCATTAAATGCT 120







;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO: 2822  
;; LENGTH: 413  
;; TYPE: DNA  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-2822

Query Match 48.0%; Score 413; DB 9; Length 413;  
Best Local Similarity 100.0%; Pred. No. 4,6e-193;  
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 TTGATTCTAATAATCCGAGTATGAGTATGAGAGCGCAATTGCACTAGAAATG 219  
DB 413 TTGATTCTAATAATCCGAGTATGAGTATGAGAGCGCAATTGCACTAGAAATG 354  
QY 220 ATTCAATACATATTCATTATTCATGATGACCTACACGCGATGATATATGCA 279  
DB 353 ATTCAATACATATTCATTATTCATGATGACCTACACGCGATGATATATGCA 294  
QY 280 CGAGGAAATTAACAATCATATAATGATGATGAGTGAAGTGGATATAGCAGGTAT 339  
DB 293 CGAGGAAATTAACAATCATATAATGATGATGAGTGAAGTGGATATAGCAGGTAT 234  
QY 340 GCTTTTAACTAAAGCATTTGAAGTATGATGATGATGATGATGATGATGATGATGAT 359  
DB 233 GCTTTTAACTAAAGCATTTGAAGTATGATGATGATGATGATGATGATGATGATGAT 174  
QY 400 AAAATTAAGTTTACACGCGCTGTCATATGACAGTGTGATGATGATGATGATGATGAT 459  
DB 173 AAAATTAAGTTTACACGCGCTGTCATATGACAGTGTGATGATGATGATGATGATGAT 114  
QY 460 CAATGTTGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATA 519  
DB 113 CAATGTTGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATA 54  
QY 520 CACAAAACAAAACAGAGGATTAATTAACCTTTGCGGTTATGATGATGATGATGATGAT 572  
DB 53 CACAAAACAAAACAGAGGATTAATTAACCTTTGCGGTTATGATGATGATGATGATGAT 1

RESULT 7  
US-09-815-242-3275/C  
; Sequence 3275, Application US/09815242  
; Patent No. US2002006159A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.01A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578

;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO: 3275  
;; LENGTH: 337  
;; TYPE: DNA  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-3275

Query Match 39.1%; Score 337; DB 9; Length 337;  
Best Local Similarity 100.0%; Pred. No. 1.3e-155;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TACATATTCATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 284  
DB 337 TACATATTCATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278  
QY 285 AAAATTAACAATCATATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 344  
DB 277 AAAATTAACAATCATATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 218  
QY 345 ATTAATTAAGCATTTGAAGTATTTCAAGTATGATGATGATGATGATGATGATGATGATGAT 404  
DB 217 ATTAATTAAGCATTTGAAGTATTTCAAGTATGATGATGATGATGATGATGATGATGATGAT 158  
QY 405 AAAAGTTTACACGCGCTGTCATATGACAGTGTGATGATGATGATGATGATGATGATGATGAT 464  
DB 157 AAAAGTTTACACGCGCTGTCATATGACAGTGTGATGATGATGATGATGATGATGATGATGAT 98  
QY 465 GTTAGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATATACACAA 524  
DB 97 GTTAGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATATACACAA 38  
QY 525 AACAAAACAGAGCATTTTAATTAACCTTTGCGGTTATG 561  
DB 37 AACAAAACAGAGCATTTTAATTAACCTTTGCGGTTATG 1

RESULT 8  
US-09-864-761-24950/C  
; Sequence 24950, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecm1ca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24950
; LENGTH: 151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL117667.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
; OTHER INFORMATION: EST HUMAN HIT: AA601023.1, EVALUATE 1.00e-14
; OTHER INFORMATION: NT HIT: AJ271735.1, EVALUATE 2.00e-15
; OTHER INFORMATION: SWISSPROT HIT: P08548, EVALUATE 1.00e-05
; US-09-864-761-24950
Query Match 2.2%; Score 19; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 503 AAACCTTGGAATGATCA 521
DB 139 AAACCTTGGAATGATCA 121
RESULT 9
US-10-027-632-194294
; Sequence 194294, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
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; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194294
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-194294
Query Match 2.2%; Score 19; DB 12; Length 580;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 394 GAAGTAAATAAATAGTTC 412
DB 85 GAAGTAAATAAATAGTTC 103
RESULT 10
US-10-027-632-194295
; Sequence 194295, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194295
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-194295
Query Match 2.2%; Score 19; DB 12; Length 580;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 394 GAAGTAAATAAATAGTTC 412
DB 85 GAAGTAAATAAATAGTTC 103
RESULT 11
US-10-027-632-194294
; Sequence 194294, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
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/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 194294
/ LENGTH: 580
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-194294
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Query Match 2.2%; Score 19; DB 13; Length 580;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 394 GAAGTAAATAAAGTTC 412
Db 85 GAAGTAAATAAAGTTC 103
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RESULT 12

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US-10-027-632-194295
/ Sequence 194295, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827,129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 194295
/ LENGTH: 580
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-194295
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Query Match 2.2%; Score 19; DB 13; Length 580;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 394 GAAGTAAATAAAGTTC 412
Db 85 GAAGTAAATAAAGTTC 103
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RESULT 13

US-09-864-761-8212/c

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/ Sequence 8212, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: GE 24263.6
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 8212
/ LENGTH: 600
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AL117667.2
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.7
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.1
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
US-09-864-761-8212
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Query Match 2.2%; Score 19; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 503 AACCTTGAATGATACA 521
Db 470 AACCTTGAATGATACA 452
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## RESULT 14

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US-10-027-632-21738
; Sequence 21738, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21738
; LENGTH: 922
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-21738
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Query Match 2.2%; Score 19; DB 12; Length 922;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 299 ATAAAGTATATGTTGAGTG 317
DB 803 ATAAAGTATATGTTGAGTG 821
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## RESULT 15

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US-10-027-632-21739
; Sequence 21739, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21739
; LENGTH: 922
```

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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-21739
```

```
Query Match 2.2%; Score 19; DB 12; Length 922;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 299 ATAAAGTATATGTTGAGTG 317
DB 803 ATAAAGTATATGTTGAGTG 821
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Search completed: November 29, 2003, 18:05:31
Job time : 340 secs
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QY 421 CTGTCATAGCAAGTGGTCATGTTGGAATGGTCGGCGGTCAATATGTTAGATGCAAGC 480  
DB 421 CTGTCATAGCAAGTGGTCATGTTGGAATGGTCGGCGGTCAATATGTTAGATGCAAGC 480  
QY 481 GAAGGCCAACCAATTGATCTTGAACCTTGGAAAATGATACCAAAACAAAACAGAGCA 540  
DB 481 GAAGGCCAACCAATTGATCTTGAACCTTGGAAAATGATACCAAAACAAAACAGAGCA 540  
QY 541 TTATTAATCTTTGGGTTATGAGTCAGCAGATATCGCTAATGTCATGATGACACTAAA 600  
DB 541 TTATTAATCTTTGGGTTATGAGTCAGCAGATATCGCTAATGTCATGATGACACTAAA 600  
QY 601 GAACATTAGGAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 601 GAACATTAGGAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 661 TTAGACTGCTATGCTGATGAGCAAAAGTTAGTAAAAAGTGGCAGCAGATCTTGAAT 720  
DB 661 TTAGACTGCTATGCTGATGAGCAAAAGTTAGTAAAAAGTGGCAGCAGATCTTGAAT 720  
QY 721 AATTAAGTACGTACGTGATGTTTATGAGGAAAGATGCGCAGAAATTAATGACTTAT 780  
DB 721 AATTAAGTACGTACGTGATGTTTATGAGGAAAGATGCGCAGAAATTAATGACTTAT 780  
QY 781 CATAGAGCAGCAGAGTGAATGAACTAACGCAATTTGATGAACTTAACTAACAC 840  
DB 781 CATAGAGCAGCAGAGTGAATGAACTAACGCAATTTGATGAACTTAACTAACAC 840  
QY 841 TTATTAAGAAATCGTTGATTTA 861  
DB 841 TTATTAAGAAATCGTTGATTTA 861

RESULT 2  
US-09-134-001C-334  
; Sequence 334, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 334  
; LENGTH: 909  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-334

Query Match 52.2%; Score 449.8; DB 4; Length 909;  
Best Local Similarity 70.2%; Pred. No. 2e-100;  
Matches 604; Conservative 0; Mismatches 257; Indels 0; Gaps 0;

QY 1 ATGACGAATCTACCGATGAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 60  
DB 28 ATGACGAATCTACCGATGAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 87  
QY 61 ATTAATTAATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
DB 88 ATCAATCATCATCATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 147  
QY 121 GAGAGTAAAGCATCCAGCAAGTCTGTATTAATTAATTAATTAATTAATTAATTAATTAAT 180  
DB 148 GAGTGTAAAGCAATCAACAGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 207  
QY 181 TATGAGTTAGTATGAAGAGCGCAATTCAGTAATTAATTAATTAATTAATTAATTAATTAAT 240

DB 208 TATCAACAAAGCACTAATAATAGCTTTAGCATGGAATGATTAATTAATCTTTAAT 267  
QY 241 CATGATGACTTACCAAGGATGATTAATGATGATTAATGACAGAGAAATTAACAAATCAT 300  
DB 268 CATGATGATTAATCAAGCAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 327  
QY 301 AAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
DB 328 AAGTATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 387  
QY 361 GAACTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 388 GAATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 447  
QY 421 CTGTCATAGCAAGTGGTCATGTTGGAATGGTCGGCGGTCAATATGTTAGATGCAAGC 480  
DB 448 CTTCACAAAGCAAGTGGTCATGTTGGAATGGTCGGCGGTCAATATGTTAGATGCAAGC 507  
QY 481 GAAGGCCAACCAATTGATCTTGAACCTTGGAAAATGATACCAAAACAAAACAGAGCA 540  
DB 508 GAAGGCCAACCAATTGATCTTGAACCTTGGAAAATGATACCAAAACAAAACAGAGCA 567  
QY 541 TTATTAATCTTTGGGTTATGAGTCAGCAGATATCGCTAATGTCATGATGACACTAAA 600  
DB 568 TTATTAATCTTTGGGTTATGAGTCAGCAGATATCGCTAATGTCATGATGACACTAAA 627  
QY 601 GAACATTAGGAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 628 AAAAAATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687  
QY 661 TTAGACTGCTATGCTGATGAGCAAAAGTTAGTAAAAAGTGGCAGCAGATCTTGAAT 720  
DB 688 CTGATGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747  
QY 721 AATTAAGTACGTACGTGATGTTTATGAGGAAAGATGCGCAGAAATTAATGACTTAT 780  
DB 748 CATTAAGTACGTACGTGATGTTTATGAGGAAAGATGCGCAGAAATTAATGACTTAT 807  
QY 781 CATAGAGCAGCAGAGTGAATGAACTAACGCAATTTGATGAACTTAACTAACAC 840  
DB 808 CATCAATATCTTCTATGAACTGCTTAATCAAAATTTCTGATCAATATGATCTTCTGAA 867  
QY 841 TTATTAAGAAATCGTTGATTTA 861  
DB 868 TTATTAAGAAATCGTTGATTTA 888

RESULT 3  
US-09-107-532A-3070  
; Sequence 3070, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:



Db	89	GGCCGGCCGAAGTTGAAAAAGCGGATGGCGTACTCATTTGAGAGCGCGGCGAAGCAATCC	148
Qy	137	GACCAGTTCCTGTTATTACTACCTTAAGATTCACTAAATACCGATATGATTAAGTATGA	196
Db	149	GTCCGTTGCTGCTTGTCACCGATTACAGCGCTCGGCAAAAGACCGGGGGTGCATTCG	208
Qy	197	AGAGCGCAATTGCACTAGAAATGATTCATACATATTCACTTATTCATGATGACTTACAG	256
Db	209	CCGTGGCCCTGCCGATTTGAATGATCCATACCGACTCTTTGATTCATGATGATTTGCCGA	268
Qy	257	CGATGATTAATGATTAATTCGACGAGGAAATTAACAATCAATAAGTATATGAGAGT	316
Db	269	GCATGACAAACGATGATTTTGGCGCGGGGGAAGCCGACGAACCAATTAAGTTCGGCGAGG	328
Qy	317	GGACTGCGATATTAGACGGTGAATGCTTTATTAACTAAGACTTGAACCTAATTC-----	371
Db	329	CGATGGCCATCTTTGGCGGGGAGCGGGTGTGACGTAACGCGTTTCAATTATCATCCGAAA	388
Qy	372	-AAGTATGATGATTAATTAATCGATGAAATTAATAAAGTTTCTACAACGGCTGTCAATAG	430
Db	389	TGCAAGATGAGGCAATCCCTCCTCCGTCCGCTTCCGCTCATCGAAGCGCTGGCGAAG	448
Qy	431	CAAGTGCTCATGTTGGAATGTCGGCGGTCAAATGTTAATATGCAAAAGCGAAGCCCAAC	490
Db	449	CGGCGGATCCGGAAGGATGTGTCGCGGTCAAGCACCGATATGAAAGAGAGAGGAGAAA	508
Qy	491	CAATTGATTTTGAACCTTGGAAATATATACACAAAACAAAACAGAGACTTATTAACTT	550
Db	509	CGCTACCGTTTCGGAGCTCGAATATCACTTCATCGCATTAACCGGGAAATCTCTGCAT	568
Qy	551	TTGCGGTTATGATGTCAGACAGATATCGCTAATGTCANTGATACACTTAAGAACATTTAG	610
Db	569	ACAGGCTGACGCGCGGCTTGATGCGGCGCTAATGCCGCGAAACCGGGAGCTTG	628
Qy	611	AAAGTTATGATTATCATTTAGGATGATGTTCCAGATTAAAGTGAATTTATTAAGACTCT	670
Db	629	ACGATTTGCGCGCCATCTAAGGCTTGACCTTTAAATTTGCGCATGATATCTCGATTTG	688
Qy	671	ATGTGATGACCAAAAGTTAGTAAAAAAAGTGCGACGCGATCTTTGAAATTAATTAAGTA	730
Db	689	AAGGGGCGAATAAAAAATCGGCACCGGTGCGGACGCGACCAAGCAACAAACAAAGCGA	748
Qy	731	CGTACGTAGTTTATTAGGAAAAGATGGCGGACGAAGTAAATGACTTATCATAGAGACG	790
Db	749	CGTATCCAGCGTTGCTGTGCTTGCCGCGCGCAAGAAAGTGGCGTTCATATCGAGG	808
Qy	791	CAGC 794	
Db	809	CGGC 812	

RESULT 5  
US-08-333-321-1  
Sequence 1, Application US/08333321  
Patent No. 5786192  
GENERAL INFORMATION:  
APPLICANT: Otsuka, Shusei  
TITLE OF INVENTION: FARNESYL PYROPHOSPHATE SYNTHETASE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edward W. Graesson, Esq.  
STREET: 1 Broadway  
CITY: New York  
STATE: N.Y.  
COUNTRY: U.S.A.  
ZIP: 10004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: No. 5786192epad, Windows 3.1  
CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/08/333,321
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/953,424
: FILING DATE: 29-SEP-1992
: APPLICATION NUMBER: JP 3-253788
: FILING DATE: 01-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Greason, Edward W.
: REGISTRATION NUMBER: 18,918
: REFERENCE/DOCKET NUMBER: 077670/00310
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 425-7200
: TELEFAX: (212) 425-5288
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 893 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Bacillus stearothermophilus
:
US-08-333-321-1

Query Match      18.1%; Score 155.6; DB 1; Length 893;
Best Local Similarity 50.9%; Pred. No. 5e-29;
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1

QY      17  TGAATTAATTATAGTATGAATCATATATGAATTATCGGTTCCGATAAATAATAGTAA 76
DB      29  TCAACGACAAAACAGCGGGTGGAAACAGCGCTCTCCGTTATATAGCGCGTTAAG 88
QY      77  TGGATACCTCAGCTAGAAAGAAATGTTGTTATTCATTAAATGCTGAGGTAACCATCC 136
DB      89  GCGCGCGCAACTGAAAAGCGCATGGGTCCTCAATTGAGCGCGCGCAACGATCC 148
QY      137  GACCAGTTCGTATTATCTACTCACTTATGATCACTAAATACGAGTATGATGATGATGA 196
DB      149  GTCCGTCCTGCTCTGTCTCCACCGTTCCGGCGCTCGGCAAGACCGCGCGCTGGATGTC 208
QY      197  AGAGGCAATGCACTAGAAATGATTCATCATATTCATCTTATATGATGATGATCCAG 256
DB      209  CCGTGCCTGGCGGATGAAATGATCCATACGTACTCTTTGATTCATGATGATTTGCCA 268
QY      257  CGATGATATATGATGATATTCGACGAGGAAATTAACAATCATTAAGTAATGATGAGT 316
DB      269  GCATGACAAACGATGATTTGGCGCGCGCGCAACCGACGACATTAAGTTGTTCCGCGAG 328
QY      317  GGACTGCATATTAGCAGGTGATGCTTTATTAACTAAAGCATTTGAATTTTC----- 371
DB      329  CGATGGCCATCTTGGCGGGGACGGGTTGTTGACGCTACGCGTTCAATTGATCACGAAA 388
QY      372  -AAGTATGATATGATTAATCTGATGAAGTAAAAATTAAGTTTACAACGGCTGTCAATG 430
DB      389  TCGAAGATGAGCGCATCCCTCCCTCCGTCGCGCTTCGAGTCAATGCAACGGCTGGGAA 448
QY      431  CAAATGATGATGTTGAAATGATGCGCGGTCGCAAAATGTTAGATATGCAAGCGAAGC 490
DB      449  CGCGCGGTCGGAAGGATGGTGGCGGTCGAGCGACGCGGATATGAAAGAGGGGAAAA 508
QY      491  CAATTGATCTTGAAACTTTGCAAAATGATACCAAAACAAAAACAGAGCATTTATTA 550
DB      509  CGCTGACGCTTTCCGAGCTCGAATACATTACATCGGCATTAATAACGGGAAAAATG 568
QY      551  TTGCGGTTATGATGACAGCAATATCGCTAATGTCGATGATCAACTAAAGAACATT 610
DB      569  ACAGGTGACAGCGCGCGCTTTGATCGCGCGCGCTGATGCGCGGCAACGCGGAGCT 628
QY      611  AAAGTTATAGTATATATTAAGTATGATGTTCCATTAAGATTAAGATTTATAGCTG 670
DB      629  ACGAATTCGCGCCCATCTAGGCTTTCGCTTTCAAAATTCGATATATTTCTGATATT 688

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QY 671 ATGTGATGAGCAAAAGTATAGTAAAGGAGGACGATCTTGAATAATATTAAGTA 720  
Db 689 AAGGGGAGAGAAAATAATCGGACAGCGGTCGCGACGACCAAGCAACAAGACGA 748  
QY 731 CGTACGTGATTTATTATGAGGAAAGATGCGCAGAGATTAATGACTTATCATAGACG 790  
Db 749 CGTATCCAGCGTTGCTGCTGCTGCGCGCGAGGAAAAGTTGGCGTTCATATCGAGG 808  
QY 791 CAGC 794  
Db 809 CGGC 812

RESULT 6  
US-08-534-910B-2  
Sequence 2, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 894 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-2

Query Match 18.1%; Score 155.6; DB 1; Length 894;  
Best Local Similarity 50.9%; Pred. No. 5e-29;  
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

QY 17 TGAATAAATTATATGATGAGTCAATATATGATTCGTTGCGATTAATAATCACTAA 76  
Db 29 TCAACGACGCAAAACAGGCGGTGAGAAACAGCGCTCTCTTATATATGACGCTTGAAG 88

QY 77 TGGATCTCAGCTAGAGAGAAAGATATGTTATTCATTAATGCTGAGGTAAAGCATCC 136  
Db 89 GCGCGCGAGAAAGTGAAGAAAAGCCATGCGTACATCTTGAAGCGCGCGGAAACGATCC 148  
QY 137 GACCACTCTGTTATTACTCATCTTATAGATTACTTAATAACGAGTATGATTAAGTATGA 196  
Db 149 GTCCGTTGCTGCTTCTGTCCACCGTTCAAGCGCTCGGCAAAAGACCGCGGTGCGATTGC 208  
QY 197 AGAGCGCAATGCTAGTAAGTAATGATTCATCATATTCCTATTATGATGACTTACAG 256  
Db 209 CCGTCCGCTGCGGATGAAATGATTCATACGATCTTTGATTCATGATGATTTGCGGA 268  
QY 257 CGATGATATATGATGATTAATGACAGAGAAATTAACAATCATTAAGTATGATGATG 316  
Db 269 GCATGACACATGATGATTTGCGCGCGGACGCGGACGCAACATTAAGTTTGGCGAGG 328  
QY 317 GGACTGCGATATTAGACGATGATCTTTATTAATTAAGCATTTGAACCTTATTTTC----- 371  
Db 329 CGATGCGCATCTTGGCGGGGAGCGGTTGTTGACGTAACGCTTCAATGATCACCGAA 388  
QY 372 -AAGTATGATGATTAATGATGAAAGTAAATAAAGTTCTACAAAGGCTGCAATAG 430  
Db 389 TCGACGATGAGCGCATCCCTCTCTCGTCCGCTGCGCTCATCGAACGCTGCGGAAG 448  
QY 431 CAAGTGTATGTTGAAATGATGCGCGGTCAAATGTTAATGATGAAAGGCGCAAC 490  
Db 449 CGCGCGCTCGAGAGGATGATGCGGTCAGGACCGCATATGAGAGAGGAGGAAA 508  
QY 491 CAATTGATCTTGAACCTTGGAAATGATACACAAAACAAAACAGAGCATTTATTAATT 550  
Db 509 CGCTGACGCTTTCGAGCTCGAATACATTCATCGGATTAACCGGAAAATGCTGCAAT 568  
QY 551 TTGCGGTTATGATGAGTACAGCATATGCTAATGTCATGATACATTAAGAACATTTAG 610  
Db 569 ACAGCGTGCACGCGCGGCTTGTATGCGGCGCTGATGCGGCAACCGCGGAGCTTG 628  
QY 611 AAAGTATGATTAATCATTTAGGATGATGATGTCAGATTAAGATGATTTATGACCTGT 670  
Db 629 ACGAATTCGCGCGCCCTAGGCTTTCCTTTCAATTCGCGATGATTTCTGATATTG 688  
QY 671 ATGTGATGAGCAAAAGTATAGTAAAGGAGGACGATCTTGAATAATATTAAGTA 720  
Db 689 AAGGGGAGAGAAAATAATCGGACAGCGGTCGCGACGACCAAGCAACAAGACGA 748  
QY 731 CGTACGTGATTTATTATGAGGAAAGATGCGCAGAGATTAATGACTTATCATAGACG 790  
Db 749 CGTATCCAGCGTTGCTGCTGCTGCGCGCGAGGAAAAGTTGGCGTTCATATCGAGG 808  
QY 791 CAGC 794  
Db 809 CGGC 812

RESULT 7  
US-08-534-910B-3  
Sequence 3, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington







Db 809 CGGC 812

RESULT 10  
US-09-475-304-1  
Sequence 1, Application US/09475304  
Patent No. 6225096  
GENERAL INFORMATION:  
APPLICANT: Narita, Keishi  
APPLICANT: Ishida, Chika  
APPLICANT: Takeuchi, Yoshie  
APPLICANT: Ohto, Chikara  
APPLICANT: Ohnuma, Shinichi  
APPLICANT: Nishino, Tokuzo  
TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE  
FILE REFERENCE: 77670/494  
CURRENT APPLICATION NUMBER: US/09/475,304  
CURRENT FILING DATE: 1999-12-30  
EARLIER APPLICATION NUMBER: JP 8-191635  
EARLIER FILING DATE: 1996-07-03  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 894  
TYPE: DNA  
ORGANISM: Bacillus stearothermophilus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(891)  
US-09-475-304-1

Query Match 18.1%; Score 155.6; DB 3; Length 894;  
Best Local Similarity 50.9%; Pred. No. 5e-29;  
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATAAATTAATAGATGAGTCAATATGATTAATGATGATGATTAATTAATCACTAA 76  
29 TCAACAGCAAAAGAGCGGTGAGAAACAGCGCTTCCGTTATATAGACGCTTAAAG 88  
77 TGAATACTAGCTAGAGAAAGATATGTTGATTAATTAATGCTGAGGATTAACGATCC 136  
89 GCGCGGAGAGCTGAGAAAGAGCGATGCGTACTATGAGAGCGCGGCAAAAGATCC 148  
137 GACCACTCTGTTATTAATCACTTAATGATTAATGATTAATGATTAATGATTAATG 196  
149 GTCCGTTGCTGCTTCTGTCCACCGCTTCCGCGCTCGGCAAAAGCCGCGGTGATTC 208  
197 AGAGCGCAATGCACTAGAAATGATTAATGATTAATGATTAATGATTAATGATTAATG 256  
209 CCGTCCGCTCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 268  
257 CGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 316  
269 GCAATGCAACGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 328  
317 GGAATGCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 371  
329 CGATGCGCATCTTGGCGGAGGAGCGGTGTTGAGTGAAGGATTAATGATTAATG 388  
372 -AAGTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 430  
389 TCAGACGATGAGCATCTTCCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCG 448  
431 CAAGTGTGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 490  
449 CGGCGCGCTCGGAGAGGATGATGCGCGGTGAGGAGCGGATTAATGATTAATGATTAATG 508  
491 CAATGATCTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTT 550  
509 CGCTGACGCTTTGAGAGCTGAAATTAATGATTAATGATTAATGATTAATGATTAATG 568  
551 TTGCGGTTATGATGAGGAGGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 610

Db 569 ACAGCGTGAAGCGCGGCTTATGATCGCGCGCTGATGCGCGCAAAACCGGAGCTTG 628  
611 AAGTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 670  
629 ACGAATTCGCGCGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 688  
671 ATGATGATGAAGCAAGTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 730  
689 AAGGCGCAAGAAAGAAATGCGAAGCGGTGCGGAGCGGACCAAGCAACAAAGCGA 748  
731 CGTACGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 790  
749 CGTATCAGCGTTCGTGCTGCTTCCGCGCGGAGGAGGAAAGTGGCGCTTCCATATCGAG 808  
791 CAGC 794

Db 809 CGGC 812

RESULT 11  
US-09-101-126-4  
Sequence 4, Application US/09101126  
Patent No. 6316216  
GENERAL INFORMATION:  
APPLICANT: OHTO, CHIKARA  
APPLICANT: MAKANE, HIROYUKI  
APPLICANT: NISHINO, TOKUZO  
APPLICANT: OHNUMA, SHINICHI  
APPLICANT: HIROOKA, KAZUTAKE  
TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES  
FILE REFERENCE: 77670/566  
CURRENT APPLICATION NUMBER: US/09/101,126  
CURRENT FILING DATE: 1999-04-27  
EARLIER APPLICATION NUMBER: PCT/JP97/03921  
EARLIER FILING DATE: 1997-10-29  
EARLIER APPLICATION NUMBER: JP 8-307506  
EARLIER FILING DATE: 1996-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 894  
TYPE: DNA  
ORGANISM: Bacillus stearothermophilus  
FEATURE:  
OTHER INFORMATION: 256-276 is an Asp-rich coding domain  
US-09-101-126-4

Query Match 18.1%; Score 155.6; DB 4; Length 894;  
Best Local Similarity 50.9%; Pred. No. 5e-29;  
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

17 TGAATAAATTAATAGATGAGTCAATATGATTAATGATTAATGATTAATGATTAATG 76  
29 TCAACAGCAAAAGAGCGGTGAGAAACAGCGCTTCCGTTATATAGACGCTTAAAG 88  
77 TGAATACTAGCTAGAGAAAGATATGTTGATTAATTAATGCTGAGGATTAACGATCC 136  
89 GCGCGGAGAGCTGAGAAAGAGCGATGCGTACTATGAGAGCGCGGCAAAAGATCC 148  
137 GACCACTCTGTTATTAATCACTTAATGATTAATGATTAATGATTAATGATTAATG 196  
149 GTCCGTTGCTGCTTCTGTCCACCGCTTCCGCGCTCGGCAAAAGCCGCGGTGATTC 208  
197 AGAGCGCAATGCACTAGAAATGATTAATGATTAATGATTAATGATTAATGATTAATG 256  
209 CCGTCCGCTCGGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 268  
257 CGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 316  
269 GCAATGCAACGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 328  
317 GCACTGCAATTAATGAGAGGATGATTTATTAATCAAAAGATTAATGATTAATTC----- 371





Oy	491	CAATGATCTTCAAACTTTGGAAATGATATACAAAACAAAACAGAGCATTTTAACTT	550
Db	509	CGCTACGCTTTCCGAGCTCGAATATCATTCATCGCATTAACCGGAAATCTCAAT	568
Oy	551	TTGCGGTTATGAGTGCAGCAGATATCGTAAATGTCATGATACAACCTAAAGACATTTAG	610
Db	569	ACAGGTCGACGCCGCGCCTTGATGGCGGCGCTATGCCCGGCAACCGCGGAGCTTG	628
Oy	611	AAAGTTATAGTATCATTTAGGTAGTATGATGATGTCAGATTAAAGATGATTTATAGACTGCT	670
Db	629	ACGAATTCGCCGCCCATCTAGAGCCTTGCCCTTCAATTCGCGATGATATCTCGATATTG	688
Oy	671	ATGTGTATGAGAACAAAGTTAGGTAAAAAAAGTGCGCGCATCTTGAAATATATAAAGTA	730
Db	689	AAGGGGCGAAMAAAAAATCGGCAGCCGCTCGGCGCGCAACCAACAAACAAAGCCG	748
Oy	731	CGTACGTAGTTATTAGGGAAGAAGTGGGCGAAGATATAATGACTTATCATAGAGCG	790
Db	749	CGTATCCAGCGTTGCTGTCGCTTGGCCGCGCAGAGAAAGATGGCGTTCATATCGAGG	808
Oy	791	CAGC 794	
Db	809	CGGC 812	

**RESULT 15**

US-09-217-609A-28  
; Séquence 28, Application US/09217609A

GENERAL INFORMATION: MURAMATSU, Masayoshi  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KORYAMA, Tanetoshi  
APPLICANT: SHIMITSU, Naoto  
APPLICANT: CHO, Yewlin  
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
? SOFTWARE: WordPerfect 6.1 for Windows
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/217,609A

```

CLASSIFICATION:  
PRIOR APPLICATION DATA: 08/873,235  
APPLICATION NUMBER: 08/873,235  
FILING DATE: 11-Jun-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: TOFFENETTY, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 10235/J  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-1776  
TELEFAX: 202-429-0796

```

? INFORMATION FOR SEQ ID NO: 28
? =====
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 486 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: single
?     TOPOLOGY: linear
?     MOLECULE TYPE: genomic DNA
?
?
? US-09-217-609A-28

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Query Match	17.5%	Score 150.6;	DB 3;	Length 486;
Best Local Similarity	58.4%;	Pred. No. 7.2e-28;		
Matches 277; Conservative	0;	Mismatches 194;	Indels 3;	Gaps 1;

Qy	121	GGAGGTAAACCCATCCGACAGTCTGTATATACACATTGATTCATAAATACCGAG	180
Db	1	GGTGGCAAGCCATTAGACCATTTACTCTTTCGACTACTTTAGATAGTTAGTGGCAAT	60
Qy	181	TATGATTTAGTATGAMAGCGCCAAATTGCATAGAAATGATTCATACATATTCCTTATT	240
Db	61	GCACATGACGGTATTACCATTTTGGCATTTGGCAGCTTGAAATGATTCATACGATATCTTTAAATT	120
Qy	241	CATGATGACCCACCAGCGATGATPATGATGATTTATGCACGAGAAATTTAAACATCAT	300
Db	121	CACATGATCTTCCGGGCATGATGATATATGATGATCTTCTCCGGTAACTCACGATTCAT	180
Qy	301	AAAGTATATGTTGAGTGCATCTGCATATTTAGCAGGTGATGCTTTTATTACTAAAGCATTT	360
Db	181	AAGGTTTGTATGAAAGCAACAGCTATATCTCGCTGGAGATGCATTCCTCATGATGCTTTT	240
Qy	361	GAATTTATTTCAAGTATGATAGATTTAACTGATGAATTTAAATTTAAAGTTCTACACGG	420
Db	241	CAATGCAATTTTAA--ATACGCAAGTTTAAACGCAAAATTTAAATTTATCATTTGATTAATTTA	297
Qy	421	CTGTCAATAGCAAGTGTGATGTTGATGATGTCGGCGGTCTCAAAATTTAGATATGCAAAAC	480
Db	298	TTAGTACTGCTTCTGATCTTAATGCAATGTTTAAAGCCAAATCTCGATATGCAAGGT	357
Qy	481	GAAGGCCAACCAATTGATCTTGAATCTTTGAATGATATACAAACAAACAAACAGAGCA	540
Db	358	GAACATTAACCATTCAGACATTTAAATGAATGGAACGATATTCATTCATTAACCCGGTGAN	417
Qy	541	TTATTAATCTTTGGGGTTATGAGTGCAGACAGATATCGCTAATGTGATGATACGA	594
Db	418	TTGATTTGTCGACGCAANTTTGATAGTGCAGGTATCATATGANTTTTTAATGATGCA	471

Search completed: November 29, 2003, 15:05:34  
Job time : 76 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: November 29, 2003, 13:30:00 ; Search time 335 Seconds

(without alignments)  
8467.845 Million cell updates/sec

Title: US-09-925-637-63

Perfect score: 861

Sequence: 1 atgagcaatctacgcgatgaa.....tattgaatcgttgattta 861

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
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15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861	100.0	861	10	US-09-925-637-63
2	861	100.0	861	14	US-10-084-205-63
3	861	100.0	1893	8	US-08-781-986A-155
4	846.6	98.3	882	9	US-09-815-242-8485
5	831.6	96.6	864	9	US-09-815-242-4184
6	413	48.0	413	9	US-09-815-242-2822
7	337	39.1	337	9	US-09-815-242-3275
8	196.8	22.9	882	9	US-09-815-242-6533
9	195	22.6	7528	10	US-09-070-927A-55
10	164	19.0	811	10	US-09-974-300-1015
11	131.4	15.3	888	9	US-09-815-242-7142
12	131.4	15.3	1830121	14	US-10-329-960-1
13	124.8	14.5	876	9	US-09-815-242-9175
14	124.2	14.4	876	9	US-09-815-242-9499
15	114.2	13.3	640681	10	US-09-790-988-1
16	102.4	11.9	900	9	US-09-815-242-5972

17	102.4	11.9	900	12	US-10-006-909-11	Sequence 11, Appl
18	102.4	11.9	5963	12	US-10-006-909-13	Sequence 13, Appl
19	98.6	11.5	891	10	US-09-934-903-13	Sequence 13, Appl
20	98.6	11.5	891	10	US-09-934-868-71	Sequence 11, Appl
21	98.6	11.5	891	11	US-09-941-947A-19	Sequence 19, Appl
22	97.8	11.4	900	9	US-09-815-242-9986	Sequence 9986, Ap
23	89.6	10.4	936	9	US-09-815-242-4260	Sequence 4260, Ap
24	89.6	10.4	969	9	US-09-815-242-8505	Sequence 8505, Ap
25	88.6	10.3	819	10	US-09-925-637-65	Sequence 65, Appl
26	88.6	10.3	819	10	US-10-084-205-65	Sequence 65, Appl
27	88.6	10.3	884	8	US-08-781-986A-185	Sequence 185, Appl
28	79.6	9.2	498	10	US-09-070-927A-509	Sequence 509, Ap
29	77.4	9.0	498	10	US-09-974-300-5453	Sequence 5453, Ap
30	76	8.8	498	10	US-09-974-300-5438	Sequence 5438, Ap
31	75.2	8.7	1268	13	US-10-108-915-17	Sequence 17, Appl
32	73.4	8.5	2000	10	US-09-887-576-115	Sequence 115, Appl
33	63.8	7.4	1470	13	US-10-108-915-25	Sequence 25, Appl
34	60.8	7.1	912	9	US-09-815-242-7285	Sequence 7285, Ap
35	60.4	7.0	1062	13	US-10-108-915-15	Sequence 15, Appl
36	60.4	7.0	1087	12	US-10-349-508-15	Sequence 15, Appl
37	60	7.0	1161	13	US-10-108-915-37	Sequence 37, Appl
38	57.4	6.7	1441	13	US-10-108-915-21	Sequence 21, Appl
39	56.6	6.6	1131	10	US-09-934-778-1	Sequence 1, Appl
40	55.6	6.5	912	11	US-09-941-947A-25	Sequence 25, Appl
41	55.6	6.5	912	12	US-10-218-118-1	Sequence 1, Appl
42	54.2	6.3	981	13	US-10-349-508-18	Sequence 18, Appl
43	50.8	5.9	993	13	US-10-108-915-23	Sequence 23, Appl
44	49.6	5.8	912	9	US-09-815-242-7450	Sequence 7450, Ap
45	48.4	5.6	888	9	US-09-815-242-7873	Sequence 7873, Ap

## ALIGNMENTS

RESULT 1  
US-09-925-637-63  
Sequence 63, Application US/09925637  
Patent No. US20020103338A1  
GENERAL INFORMATION:  
APPLICANT: Choi  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: PB560  
CURRENT APPLICATION NUMBER: US/09/925,637  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/151,933  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781,986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956,171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009,861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 63  
LENGTH: 861  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-637-63  
Query Match 100.0%; Score 861; DB 10; Length 861;  
Best Local Similarity 100.0%; Pred. No. 3.7e-175;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 ATGAGCAATCTCCGATGAATTAATTAAGTGAAGCAATTAATGAATTCGGTGGC 60  
1 ATGAGCAATCTCCGATGAATTAATTAAGTGAAGCAATTAATGAATTCGGTGGC 60  
61 ATAAATTAATCAGTATGATCTACGCTAGAGAAGATGATGTTATTCATTAAATGCT 120  
61 ATAAATTAATCAGTATGATCTACGCTAGAGAAGATGATGTTATTCATTAAATGCT 120

QY 121 GGAGGTAAAGCATCCGACGAGTTCGTATTAATCACTTAAGTTCATTAATACCGAG 180  
Db 121 GGAGGTAAAGCATCCGACGAGTTCGTATTAATCACTTAAGTTCATTAATACCGAG 180  
QY 181 TATGAGTAAAGTAAAGAGCGCAATTCAGTAAGAAATGATTCATTAATACCGAG 240  
Db 181 TATGAGTAAAGTAAAGAGCGCAATTCAGTAAGAAATGATTCATTAATACCGAG 240  
QY 241 CATGATGACCTACGAGGATGATTAATGATGATTAATGAGGAAATTAACCAATCAT 300  
Db 241 CATGATGACCTACGAGGATGATTAATGATGATTAATGAGGAAATTAACCAATCAT 300  
QY 301 AAGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 360  
Db 301 AAGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 360  
QY 361 GAACCTATTTCAAGTGAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 420  
Db 361 GAACCTATTTCAAGTGAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 420  
QY 421 CTGTCAATGACCAAGTGTGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 480  
Db 421 CTGTCAATGACCAAGTGTGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 480  
QY 481 GAAGGCCAACCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 540  
Db 481 GAAGGCCAACCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 540  
QY 541 TTATTAATTTTGGGTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 600  
Db 541 TTATTAATTTTGGGTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 600  
QY 601 GAACATTTAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 660  
Db 601 GAACATTTAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 660  
QY 661 TTGACCTGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 720  
Db 661 TTGACCTGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 720  
QY 721 AATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 780  
Db 721 AATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 780  
QY 781 CATGAGACGACGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 840  
Db 781 CATGAGACGACGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 840  
QY 841 TTATTAAGAAATCGTTGATTTA 861  
Db 841 TTATTAAGAAATCGTTGATTTA 861

## RESULT 2

US-10-084-205-63  
; Sequence 63, Application US/10084205  
; Publication No. US20030049648A1  
; GENERAL INFORMATION:  
; APPLICANT: Choi, Gil  
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides  
; FILE REFERENCE: P515P1  
; CURRENT APPLICATION NUMBER: US/10/084,205  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: PCT/US00/23773  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/151,933  
; PRIOR FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 63  
; LENGTH: 861  
; TYPE: DNA

ORGANISM: Staphylococcus aureus  
US-10-084-205-63

Query Match 100.0%; Score 861; DB 14; Length 861;  
Best Local Similarity 100.0%; Pred. No. 3.7e-175;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGATCTACCGATGAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 60  
Db 1 ATGACGATCTACCGATGAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 60  
QY 61 ATTAATTAATCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 120  
Db 61 ATTAATTAATCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 120  
QY 121 GGAGGTAAAGCATCCGACGAGTTCGTATTAATCACTTAAGTTCATTAATACCGAG 180  
Db 121 GGAGGTAAAGCATCCGACGAGTTCGTATTAATCACTTAAGTTCATTAATACCGAG 180  
QY 181 TATGAGTAAAGTAAAGAGCGCAATTCAGTAAGAAATGATTCATTAATACCGAG 240  
Db 181 TATGAGTAAAGTAAAGAGCGCAATTCAGTAAGAAATGATTCATTAATACCGAG 240  
QY 241 CATGATGACCTACGAGGATGATTAATGATGATTAATGAGGAAATTAACCAATCAT 300  
Db 241 CATGATGACCTACGAGGATGATTAATGATGATTAATGAGGAAATTAACCAATCAT 300  
QY 301 AAGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 360  
Db 301 AAGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 360  
QY 361 GAACCTATTTCAAGTGAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 420  
Db 361 GAACCTATTTCAAGTGAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 420  
QY 421 CTGTCAATGACCAAGTGTGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 480  
Db 421 CTGTCAATGACCAAGTGTGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 480  
QY 481 GAAGGCCAACCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 540  
Db 481 GAAGGCCAACCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 540  
QY 541 TTATTAATTTTGGGTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 600  
Db 541 TTATTAATTTTGGGTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 600  
QY 601 GAACATTTAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 660  
Db 601 GAACATTTAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 660  
QY 661 TTGACCTGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 720  
Db 661 TTGACCTGATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 720  
QY 721 AATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 780  
Db 721 AATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 780  
QY 781 CATGAGACGACGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 840  
Db 781 CATGAGACGACGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 840  
QY 841 TTATTAAGAAATCGTTGATTTA 861  
Db 841 TTATTAAGAAATCGTTGATTTA 861

## RESULT 3

US-08-781-986A-155/c  
; Sequence 155, Application US/08781986A  
; Publication No. US20030054436A1  
; GENERAL INFORMATION:









Db 277 AAAATTAACAATCATTAAGTATATGTGAGTGAAGCTGCAATATTAGCAGGTGATGCTTT 218  
Qy 345 ATTAACTAAGCATTTGAATCTTAAAGTATGATGATTAATCTGATGAAGTAAAT 404  
Db 217 ATTAACTAAGCATTTGAATCTTAAAGTATGATGATTAATCTGATGAAGTAAAT 158  
Qy 405 AAAAGTTCTACAGCGCTGTCAATAGCAAGTGTCAATGTTGAAATGTCGCGGTCAAT 464  
Db 157 AAAAGTTCTACAGCGCTGTCAATAGCAAGTGTCAATGTTGAAATGTCGCGGTCAAT 98  
Qy 465 GTTAGATATGCAAGGAGGAGCCCAACCAATGATCTTGAACCTTGGAAATGATACAA 524  
Db 97 GTTAGATATGCAAGGAGGAGCCCAACCAATGATCTTGAACCTTGGAAATGATACAA 38  
Qy 525 AACAAAAACAGACATTAATTAATCTTGGCGGTATG 561  
Db 37 AACAAAAACAGACATTAATTAATCTTGGCGGTATG 1

RESULT 8  
US-09-815-242-6533  
Sequence 6533, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zykend, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815.242  
PRIORITY FILING DATE: 2001-03-21  
PRIORITY APPLICATION NUMBER: 60/191,078  
PRIORITY FILING DATE: 2000-03-21  
PRIORITY APPLICATION NUMBER: 60/206,848  
PRIORITY FILING DATE: 2000-05-23  
PRIORITY APPLICATION NUMBER: 60/207,727  
PRIORITY FILING DATE: 2000-05-26  
PRIORITY APPLICATION NUMBER: 60/242,578  
PRIORITY FILING DATE: 2000-10-23  
PRIORITY APPLICATION NUMBER: 60/253,625  
PRIORITY FILING DATE: 2000-11-27  
PRIORITY APPLICATION NUMBER: 60/257,931  
PRIORITY FILING DATE: 2000-12-22  
PRIORITY APPLICATION NUMBER: 60/269,308  
PRIORITY FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 6533  
LENGTH: 882  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(882)  
US-09-815-242-6533

Query Match 22.9%; Score 196.8; DB 9; Length 882;  
Best Local Similarity 56.1%; Pred. No. 1,4e-32;  
Matches 413; Conservative 0; Mismatches 317; Indels 6; Gaps 2;

Qy 92 AAGAAAGATGTGTATTCATTAATGCTGAGGTAACCGCATCCGACAGTTCTGTTAT 151  
Db 89 AAGAAAGATGTGTATTCATTAATGCTGAGGTAACCGCATCCGACAGTTCTGTTAT 148  
Qy 152 TACTACTTATGATTCATTAATGCGAGTATGA---GTAGTATGAAGAGCGCAATTG 208  
Db 149 TAACAAACAGTGGCGCTTTTCAAAAAGATGAAAGCAAGCAACTATCAAGTGGCT 208

Qy 209 CACTAAGATGATTCATACATATTTCACTTATTCATGATGACCTACAGCGATGATATG 268  
Db 209 CTTAGAGATGATTCATACATATTTCACTTATTCATGATGATTTACAGCAATGATATG 268  
Qy 269 ATGATTAATGCAAGAGAAAATTAACAATCATTAAGTATGATGATGATGATGAT 328  
Db 269 ATGATTAATGCAAGAGAAAATTAACAATCATTAAGTATGATGATGATGATGATGAT 328  
Qy 329 TAGCAGTATGCTTTATTTAATTAAGCAATTTGAACCTTATTTCAAGTATGATTA 388  
Db 329 TAGCAGTATGCTTTATTTAATTAAGCAATTTGAACCTTATTTCAAGTATGATTA 385  
Qy 389 CTGATGAAGTAAATTAAGATTTCAACAGCGCTGTCAATAGCAAGTGTCTGTTGAA 448  
Db 386 GCTTAAGTAAATTAAGATTTCAACAGCGCTGTCAATAGCAAGTGTCTGTTGAA 445  
Qy 449 TGGTCGCGGTCAATGTTAATATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 508  
Db 446 TGGTCGCGGTCAATGTTAATATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 505  
Qy 509 TGGAAATGATACACAAACAAACAGAGGACATTTAATCTTTGCGGTATGATGAC 568  
Db 506 TAGCGGCTGTTCATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 565  
Qy 569 CAGATATGCTATATGCTATGATGATCAACCTAAGAGGAGGAGGAGGAGGAGGAGG 628  
Db 566 GCGTATTAAGCAATCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 625  
Qy 629 TAGTATGATGTTCCAGATTAAGATTAATTAATTAATTAATTAATTAATTAATTA 688  
Db 626 ATGGCTTGGCTTTTCAATTCGATGATGATGATGATGATGATGATGATGATGATG 685  
Qy 689 TAGTATTAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 748  
Db 686 TAGTATTAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 745  
Qy 749 GGAAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 808  
Db 746 GGAATGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 805  
Qy 809 CGCAATTTGATGAACA 824  
Db 806 AAAAATCAAGCAAA 821

RESULT 9  
US-09-070-927A-55  
Sequence 55, Application US/09070927A  
Patent No. US20020120116A1  
GENERAL INFORMATION:  
APPLICANT: Charles A. Kunsch  
APPLICANT: Patrick J. Dillon  
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070.927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,655  
FILING DATE: 1997-05-16  
APPLICATION NUMBER: 60/044,031  
FILING DATE: 1997-05-06  
APPLICATION NUMBER: 60/066,009  
FILING DATE: 1997-11-14  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: P9369  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7528 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-09-070-927A-55

Query Match 22.6%; Score 195; DB 10; Length 7528;  
Best Local Similarity 56.9%; Pred. No. 7.5e-32;  
Matches 398; Conservative 0; Mismatches 295; Indels 6; Gaps 2;

92 AAGAAATATGTTGTTATTCATTAATCTGAGGTAAGCCATCCAGCCAGTTCTGTAT 151  
6730 AAGAGCAATGCTCTACTCATACACCGAGTGGCAACGATTACGCCCTTATGTGT 6789

152 TACTCCTTAGATCTCTAATAACGAGTATGA---GTTAGATGAAGAGGCAATTG 208  
6790 TAACAACAGTGGCCGCTTTCACAAAAGATGAACAACAAGCTATCAAGTGGCTCCT 6849

209 CACTAGAAATGATTCATACATATTCATTCATGATGACTACACGAGTGGATATG 268  
6850 CTTTAGAGATGATTCATACGATTCATTAATCATGATGATTTACACGAAATGAGCATG 6909

269 ATGATTTACGACGAGAAATTAACAATCATTAAGTATGTTAGTGGAGCTGGCATAT 328  
6910 ATGATTTACGCTGGGCAACCAACATTAAGTGTGGTGAAGCGACCTGCCATTT 6969

329 TACAGAGTATGCTTTTATTAACATTAAGCATTTGAACCTATTTCAGATGATAGATTA 388  
6970 TACAGAGGACGCGCTTATTAACAGGTGCTATTCAGTTGCTTC---TTGAGTCAATTAG 7026

389 CTGATGAGTAAATAATAAGTTCTACACGCGCTGCAATAGCAAGTGCATGTTGAA 448  
7027 GCTTAAGTGAATAAGTTTACTGATGCAACACTGGCAAGCGGAGCAATCAAGCA 7086

449 TGGTCCGCGGTCAATGTTAGATATGCAAAAGCGAAGCCAACTGATCTTGAACTT 508  
7087 TGGTTCGCCGCAATAGGTGATATGAGAAAGCAAGTCAAGTCACTTGAAGAGT 7146

509 TGGAAATGATACCAAAACAAAACGAGCATTTATACCTTTGCGGTATAGAGCAG 568  
7147 TACCGGCTGTTCAAGAAAAGAAAACGAGCGCTTAATTGAATTCGCTTAATTGCTGGG 7206

569 CAGATATCGCTAATGTCATGATACAACTTAAGAACTTTAGAAAGTTATAGTTATCAT 628  
7207 GCGTATTAGCAATCAAAACAGAAAGTCACTTGTTCATGACACAGTTGCCCATCACT 7266

629 TAGGTATGATGTTCCAGATTAAAGATGATTATTAAGCTGATGATGAAGCAAGT 688  
7267 ATGGCTTGGCTTTCAAAATCGTATGATCTTATAGTGCACAAATGACAAAGCAGATT 7326

689 TAGGTAAATAGTGGGAGGAGCTTGAATAATAAAGTACGTACGTAGTTATAG 748  
7327 TAGGTAAATAGTGGGAGGAGTGAACGTTGAATAAAGTACGTATCCAGCTCTTCTAG 7386

749 GGAAGATGCGCAGAGATTAATGACTTATCATAG 787  
7387 GGAATGCTGGCGCAAAAGATCCGCTAACATCAATTAG 7425

RESULT 10  
US-09-974-300-1015  
Sequence 1015, Application US/09974300  
Patent No. US20020146721A1  
GENERAL INFORMATION:  
APPLICANT: Berka, Randy M.  
APPLICANT: Clausen, Ib Groth  
TITLE OF INVENTION: Methods for Monitoring Multiple Gene  
FILE REFERENCE: 10085,500-US  
CURRENT APPLICATION NUMBER: US/09/974,300  
CURRENT FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: 09/680,598  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/279,526  
PRIOR FILING DATE: 2001-03-27  
NUMBER OF SEQ ID NOS: 8481  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1015  
LENGTH: 811  
TYPE: DNA  
ORGANISM: Bacillus licheniformis  
US-09-974-300-1015

Query Match 19.0%; Score 164; DB 10; Length 811;  
Best Local Similarity 52.9%; Pred. No. 1.5e-25;  
Matches 378; Conservative 0; Mismatches 330; Indels 6; Gaps 1;

88 CTAGAAAGATATGTTGTTATTCATTAATGCTGGAGGTAACGATCCGACGATTCG 147  
97 CTCAGAGATTCATGCTGATCTATTTGAACCGGGGGAACGCTGAGACCGATTTG 156

148 TTATTACTCATCTTATGATTCATTAATACGATATAGTATGTAAGAGCGCAATT 207  
157 GTTCTTGGCTTCTTATGCTGATACGGAAGAAAGACGGAATTCAGTGGATGC 216

208 GCACTAGAAATGATTCATACATTTTCACTTATTCATGATGACTTACAGGATGATAT 267  
217 GCGGTTGAATATCATCATGATTCATTAATTCATGAGAGACTCCCTGTATGATGAC 276

268 GATGATTAACGACGAGAAATTAACAATCATTAAGTATGATGAGTGGAGATA 327  
277 GATGATCTCAAGAGATGAGCCGACAAACACAAATTTACGGGAGGCGGCAATT 336

328 TTAGCAGTATGATCTTATTAACATTAAGCATTTGAACCTTATTTCC-----AAGTATGAT 381  
337 CTCGGGAGAGCGCTTATTAACGGAAGCTTCAAAATGATCACTTCAATATGCTTCT 396

382 AGATTACTGATGAATTAATAATAAGTTCTACACGCGCTGCAATGACAGTGTCAAT 441  
397 GATGATCCGCTGAAGAGCGCATCAGATCGTGAACGAGCTATTTCCGACGCGGGGCC 456

442 GTTGAATGATGCGCGCTCAATGTTAGATGATGCAAGGAGGCGCAACATGATCTT 501  
457 GAAGGATGATGCGCGCTGATTTAGATGATGAAAGCGGAATCAAAAGTGTGATCTCT 516

502 GAACTTTGGAATGATGATACAAAACAAAACGAGCATTTATTAATTTTGGCGTTAG 561  
517 GATGAATCAGAGATTCACAGAGAAAACGCTTAATCTCTAGCTTCAAGCTCAT 576

562 AGTGACGAGATATCGCTATGTCATGATACAACTTAAGAACATTTAGAAAGTATAGT 621  
577 GCGGAGCGCATCTTTCAGATGATGATGAAAAGATGAAAAGCTGGCGGAATTCAGC 636

622 TATCATTTAGATATGATGTTCCAGATTAAGATGATTTATTTGACCTGATGATGAA 681  
637 CATCATATGCGATCGCTTTTCAAGATCAGAGATGATTTTGAACCTTGAAGCTTGGAG 696

682 GCAAACTTAGTAAATAAGTGGGAGCGATCTTGAATAATAAAGTACGTACGTAGAT 741  
697 GATTAATGCGCAAGAGATCGATCCGCTTCAACGAAAGTGCAGATATCGGTGG 756

Qy 742 TTATAGGAAAGATGGCGCAGAAATTAATGACTTATCATAGACGACGA 795  
Db 757 CTCCTTGGCTTGAGGGCGCCAGCCAAAACCTGATGACATATTGAAAAAGCA 810

## RESULT 11

US-09-815-242-7142  
; Sequence 7142, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyekind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7142  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Haemophilus influenzae  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(888)  
US-09-815-242-7142

Query Match 15.3%; Score 131.4; DB 9; Length 888;  
Best Local Similarity 49.9%; Pred. No. 1.5e-18;  
Matches 361; Conservative 0; Mismatches 356; Indels 6; Gaps 1;

Qy 100 ATGTGTTATTCATTAATGCTGGAGGTAAAGCATCCGACGATTCGTATTACTACT 159  
Db 109 ATGAAATACGATTAATTAATCTGGCGTAAGGAGTGGCCCTTCTTAGTTAGCAACA 168  
Qy 160 TTAGATTCACAAATACCGATGATGATGATGATGATGATGATGATGATGATGATG 219  
Db 169 GGTAAATGCTGGCGCAGAAACAAACCTTAGATTAAGCTGCTGCGCATGAAAGCC 228  
Qy 220 ATTGATCATTAATTCATTAATTCATGATGATGATGATGATGATGATGATGATGATG 279  
Db 229 ATTACGCGTATTCCTTAATTCAGATGATGATGATGATGATGATGATGATGATGATG 288  
Qy 280 CGAGGAAATTAACAAATCATTAAGTATGATGATGATGATGATGATGATGATGATG 339  
Db 289 CGTGAATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 348  
Qy 340 GCTTATTAATAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 399  
Db 349 GCACTGCAAAAGTTTGCATTTGAAATTTAAACCAAAACCGAATATTTCTACTGAACA 408

Qy 400 AAAATAAAGTTCTACACCGCTGTCAATAGCAAGTGTGATGTGATGTGCGGGT 459  
Db 409 AAATGCGCTTAATTCATTAATTTAGCGCAAGGGCTGTGTGCAAGAAATGTGTTAGGG 468  
Qy 460 CAAATGTTAGATATGCAAGCGCAAGGCCAACCAATGATCTTGAAACTTTGAAATGATA 519  
Db 469 CAAAGTTAGATCTTAATTTCTGAGCATTAACAGATTAAGTTAAGTAAATGATTAAT 528  
Qy 520 CACAAAACAAAACAGGAGCATTAATTAATTTGCGGTTATGATGATGATGATGATGATG 578  
Db 529 CATGCTACAAAACGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 588  
Qy 579 -----TAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 633  
Db 589 CCGATTTTACGCAACAAAGGTTAGAACATCTTAACCAATATGCGAAGCATTTGT 648  
Qy 634 ATGATGTTCCAGATTTAAAGATTTTATTTGATGATGATGATGATGATGATGATGAT 693  
Db 649 TTAGCTTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 708  
Qy 694 AAAAAGTGGCGACGATCTTGAATTAATTAAGTACGATGATGATGATGATGATGATG 753  
Db 709 AAACAGTGGTGGCCGATCTTGAATTAATTAAGTACGATGATGATGATGATGATGAT 768  
Qy 754 GATGCGCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 813  
Db 769 AGTGTGCAAAAACAAAGGCAAGATCTATATCAAAAGTGGTGTGCTGATTAAGAAAA 828  
Qy 814 ATT 816  
Db 829 ATT 831

## RESULT 12

US-10-329-960-1  
; Sequence 1, Application US/10329960  
; Publication No. US20030099277A1  
; GENERAL INFORMATION:  
; APPLICANT: Fleischmann et al.  
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag  
; FILE REFERENCE: PB186P1  
; CURRENT APPLICATION NUMBER: US/10/329,960  
; PRIOR FILING DATE: 2003-01-02  
; PRIOR APPLICATION NUMBER: US 09/643,990  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: US 08/487,429  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/426,787  
; PRIOR FILING DATE: 1995-04-21  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1830121  
; TYPE: DNA  
; ORGANISM: Haemophilus influenzae  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4747)..(4747)  
; OTHER INFORMATION: n equals a, t, g or c  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9921)..(9921)  
; OTHER INFORMATION: n equals a, t, g or c  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (10150)..(10150)  
; OTHER INFORMATION: n equals a, t, g or c  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (29298)..(29298)  
; OTHER INFORMATION: n equals a, t, g or c  
; FEATURE:

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NAME/KEY: misc_feature
LOCATION: (36543)..(36543)
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LOCATION: (122167)..(122167)
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NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
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FEATURE:
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OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145942)..(145942)
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Db 437 GATATGTCAGAGGCAAGTTTGGATATGAGGCGACCAACAGCACTTGTCTGGAAG 496  
Qy 506 CTTTGGAAATGATACCAAAAACAAAACAGAGCATTTAATCTTTGGGTTATAGG 565  
Db 497 AACTTCAGACTATTCATGCGCAATAGAGCTGGAAAGTTACTAGCTATCCCTTCAAGCG 556  
Qy 566 CAGCAGATATCGCTAATGTCGATGATACAACTAAAGCATTTAGAAAGTTAAGTTATC 625  
Db 557 CAGCTATTATAGCTAATGTCACTGAAATGAGGTGAAGCTGAAACTGTGGGTGAAT 616  
Qy 626 ATTAGATGATGTTCCAGATTAAGATGATTTATTAGACTGCTATGCTGATGAACAA 685  
Db 617 TGATTGACTTGTCTTTCAGTCAAGTCAAGATGATGTACTGATGTGACAGCTAGTTTGAAG 676  
Qy 686 AGTTAGTAAAAAAGGGGAGGAGCTTTGAAATATATAAAGTACGTACGATTTAT 745  
Db 677 AATCGGTAAAGACCTCAAAAGGATCTGAGGCAAGAAATCACTATCCTGCTTGT 736  
Qy 746 TAGGGAAGATG 757  
Db 737 TGGGCTTGAAG 748

## RESULT 14

US-09-815-242-9499 Application US/09815242  
Sequence 9499, Patent No. US20020061569A1

GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9499  
LENGTH: 876  
TYPE: DNA  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(876)  
US-09-815-242-9499

Query Match 14.4%; Score 124.2; DB 9; Length 876;  
Best Local Similarity 51.6%; Pred. No. 5.3e-17;  
Matches 335; Conservative 0; Mismatches 308; Indels 6; Gaps 2;  
Qy 89 TAGAAGAAAGTATGTTGATTCATTAATGCTGAGAGTAAAGCATCGACCGAGTTCTGT 148

Db 80 TAGGGAGTCTGTTCTCTATTCATTCATGCTGAGGCAAGGATATTCGACCTTTTCTCT 139  
Qy 149 TATTACTCCTTAGTTACTAA--TACGAGATGATAGTTAGGTATGAAGAGGCA 205  
Db 140 TGTGAAAGTTCTGGAAGCTTGACAGTTACATCAACCTGTCTACGGCAGGTAGCTA 199  
Qy 206 TTGCACTAGAAATGATTCATACATATTCATTTATCATGATGACCTACAGCGATGATA 265  
Db 200 CTGCTTGAAGATGATTCATACAGGAGGAGTGTATTCAGATGACCTTCTGTATGATG 259  
Qy 266 ATGATGATATTCAGCAGAGAAAATTAACAATCATTAAGATATATGATGATGCA 335  
Db 260 ATGACGATATTCAGAAAGAGGCGGTTTAAACCAATCAACAAGAAATTCGATGAAGTCCA 319  
Qy 326 TATTAGCAGTATGCTTTATTAATCAAGCATTTGAATTTTAAAGTATGATAGAT 385  
Db 320 TTTTGGCTGGAGATGCTTATTCATAGACCAATATGCTTGAATGCGAGGAGAA--T 376  
Qy 386 TAACGTATGATTAATAAATAAAGTTCTACAAGGCTGTCAATAGCAAGTGCATGTTG 445  
Db 377 TGCCAGTCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 436  
Qy 446 GAATGCTGCGGCTCAATGTTAGATGCAAAAGGCAAGGCAACCAATGATCTTGAA 505  
Db 437 GATGCTGAGGAGGCAAGTTTGGATATGAGAGGCGAACCAGCACTTGTCTTGAAG 496  
Qy 506 CTTTGGAAATGATACCAAAAACAAAACAGAGCATTTAATCTTTGGGTTATAGG 565  
Db 497 AACTTCAGATTAATTCATGCGCAATAGACTGGAGATTAACCTATCCCTTCAAGCG 556  
Qy 566 CAGCAGATATCGCTAATGTCGATGATACAACTAAAGCATTTAGAAAGTTAAGTTATC 625  
Db 557 CAGCTATTATAGCTAATGTCACTGAAATGAGGTGAAGCTGAAACTGTGGGTGAAT 616  
Qy 626 ATTAGATGATGTTCCAGATTAAGATGATTTATTAGCTGCTATGCTGATGAACAA 685  
Db 617 TGATTGACTTGTCTTTCAGTCAAGTCAAGATGATGTAAGTATGACAGCTAGTTTGAAG 676  
Qy 686 AGTTAGTAAAAAAGTGGCAGCGATCTTGAATATATAAAGTACGTA 734  
Db 677 AATCGGCAAGACACCTCAAAAGGATCTGAGGCAAGAAATCAACCTA 725

## RESULT 15

US-09-790-988-1/c  
Sequence 1, Application US/09790988  
Patent No. US20020127687A1  
GENERAL INFORMATION:  
APPLICANT: SHIGENOBU, SHUJI  
APPLICANT: WATANABE, HIDEMI  
APPLICANT: HATTORI, MASAHIRA  
APPLICANT: SAKAKI, YOSHIYUKI  
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
FILE REFERENCE: 081356/0159  
CURRENT APPLICATION NUMBER: US/09/790,988  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: JP2000-107160  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 640681  
TYPE: DNA  
ORGANISM: Buchnera sp.  
US-09-790-988-1

Query Match 13.3%; Score 114.2; DB 10; Length 640681;  
Best Local Similarity 51.4%; Pred. No. 8.7e-14;  
Matches 319; Conservative 0; Mismatches 293; Indels 9; Gaps 2;  
Qy 88 CTAGAAGAAAGTATGTTGATTCATTAATGCTGAGGATTAAGCATCGACCGAGTTCTG 147  
Db 511231 CTTTAAAGCAATGAATATATGATTTTTCAGGTAGTAAAGATGCGTTTCATCTTTA 511172



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:37:51 ; Search time 21 Seconds

(without alignments)  
578.248 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 287

Sequence: 1 MTNLPMNKLIDEVNNELSA.....ELQIDQGNTHLLEIVDL 287

Scoring table: OLIGO

Gapop 60.0 ; Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:  
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3: /cgn2\_6/prodata/1/aa/6A COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6B COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/PCTUS COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	35.5	293	3	US-09-276-873-2
2	37	12.9	302	4	US-09-134-001C-3171
3	17	5.9	280	4	US-09-634-238-303
4	17	5.9	312	4	US-09-107-532A-6724
5	14	4.9	297	1	US-08-534-910B-7
6	14	4.9	297	1	US-08-534-910B-8
7	14	4.9	297	1	US-08-534-910B-10
8	14	4.9	297	3	US-08-886-466-2
9	14	4.9	297	3	US-09-475-304-2
10	14	4.9	297	4	US-09-101-126-3
11	14	4.9	297	4	US-09-367-528A-5
12	11	3.8	291	3	US-09-275-742-2
13	9	3.1	320	3	US-09-217-609A-6
14	9	3.1	320	3	US-08-873-235B-6
15	8	2.8	219	4	US-09-328-352-5590
16	8	2.8	285	2	US-09-187-050-12
17	8	2.8	293	2	US-08-284-465-4
18	8	2.8	293	2	US-08-284-465-3
19	8	2.8	294	2	US-08-284-465-3
20	8	2.8	297	1	US-08-534-910B-6
21	8	2.8	297	1	US-08-534-910B-9
22	8	2.8	297	4	US-09-367-528A-1
23	8	2.8	297	4	US-09-367-528A-3
24	8	2.8	333	3	US-09-187-050-2
25	8	2.8	333	3	US-09-187-050-14
26	8	2.8	333	3	US-09-187-050-16
27	8	2.8	393	3	US-09-187-050-18

28	8	2.8	393	3	US-09-187-050-20	Sequence 20, Appl
29	8	2.8	393	3	US-09-187-050-22	Sequence 22, Appl
30	8	2.8	393	3	US-09-187-050-24	Sequence 24, Appl
31	8	2.8	393	3	US-09-187-050-26	Sequence 26, Appl
32	8	2.8	393	3	US-09-187-050-27	Sequence 27, Appl
33	8	2.8	393	3	US-09-187-050-28	Sequence 28, Appl
34	8	2.8	393	3	US-09-187-050-29	Sequence 29, Appl
35	8	2.8	393	3	US-09-187-050-30	Sequence 30, Appl
36	8	2.8	393	3	US-09-187-050-31	Sequence 31, Appl
37	8	2.8	393	3	US-09-187-050-32	Sequence 32, Appl
38	8	2.8	393	3	US-09-187-050-33	Sequence 33, Appl
39	8	2.8	393	3	US-09-187-050-34	Sequence 34, Appl
40	8	2.8	401	4	US-09-252-991A-26387	Sequence 26387, A
41	7	2.4	8	3	US-09-217-609A-7	Sequence 7, Appl
42	7	2.4	8	3	US-08-873-235B-7	Sequence 7, Appl
43	7	2.4	27	1	US-08-351-365-2	Sequence 2, Appl
44	7	2.4	27	2	US-08-467-538-2	Sequence 2, Appl
45	7	2.4	211	4	US-09-252-991A-23822	Sequence 23822, A

## ALIGNMENTS

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RESULT 1
US-09-276-873-2
; Sequence 2, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwina Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: Ispra
; FILE REFERENCE: GM10208
; CURRENT APPLICATION NUMBER: US/09/276, 873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-276-873-2

Query Match      35.5%  Score 102; DB 3; Length 293;
Best Local Similarity 100.0%; Pred No. 1.1e-92;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KLTNHRVYGEWTAIILAGDALITKAPFLISSDDRLTDEVKIKVLRSLASGHVWGGM 155
DB 96 KLTNHRVYGEWTAIILAGDALITKAPFLISSDDRLTDEVKIKVLRSLASGHVWGGM 155
QY 156 LMQSEGQPIDLETLEMHKTKTGALLTPAVMSADIADVDD 197
DB 156 LMQSEGQPIDLETLEMHKTKTGALLTPAVMSADIADVDD 197

RESULT 2
US-09-134-001C-3171
; Sequence 3171, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055, 779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3171
; LENGTH: 302
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TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3171

Query Match 12.9%; Score 37; DB 4; Length 302;  
Best Local Similarity 100.0%; Pred. No. 1.6e-28;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMHTYSLIHDDLPMANDNDYRGKLTNKKYGVEM 106  
DB 79 ALEMHTYSLIHDDLPMANDNDYRGKLTNKKYGVEM 115

RESULT 3  
US-09-634-238-303

Sequence 303, Application US/09634238  
Patent No. 6544772  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Havukkala, Ilkka J.  
APPLICANT: Bloksberg, Leonard, N.  
APPLICANT: Lubbers, Mark W.  
APPLICANT: Dekker, James  
APPLICANT: Christensson, Anna C.  
APPLICANT: Holland, Rose  
APPLICANT: O'Toole, Paul W.  
APPLICANT: Reid, Julian R.  
APPLICANT: Coolbear, Timothy  
TITLE OF INVENTION: Polynucleotides, materials incorporating  
FILE REFERENCE: 11000.104301  
CURRENT APPLICATION NUMBER: US/09/634.238  
CURRENT FILING DATE: 2000-08-08  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: FaalSeq for Windows Version 4.0  
SEQ ID NO 303  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Lactobacillus rhamnosus  
US-09-634-238-303

Query Match 5.9%; Score 17; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 8.4e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMANDND 91  
DB 70 HTYSLIHDDLPMANDND 86

RESULT 4  
US-09-107-532A-6724

Sequence 6724, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESS: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: 40,489  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277  
INFORMATION FOR SEQ ID NO: 6724:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...312  
SEQUENCE DESCRIPTION: SEQ ID NO: 6724:  
US-09-107-532A-6724

Query Match 5.9%; Score 17; DB 4; Length 312;  
Best Local Similarity 100.0%; Pred. No. 9.3e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMANDND 91  
DB 93 HTYSLIHDDLPMANDND 109

RESULT 5  
US-08-534-910B-7

Sequence 7, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBAI, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyozo  
APPLICANT: KOYAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.

REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
US-08-534-910B-7

Query Match  
Best Local Similarity 4.9%; Score 14; DB 1; Length 297;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLHDDLP 85  
DB 76 EMHTYSLHDDLP 89

RESULT 6  
US-08-534-910B-8  
Sequence 8, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl-diphosphate And Gene Coding There  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus

US-08-534-910B-8

Query Match  
Best Local Similarity 4.9%; Score 14; DB 1; Length 297;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLHDDLP 85  
DB 76 EMHTYSLHDDLP 89

RESULT 7  
US-08-534-910B-10  
Sequence 10, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl-diphosphate And Gene Coding There  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus

US-08-534-910B-10

Query Match  
Best Local Similarity 4.9%; Score 14; DB 1; Length 297;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLHDDLP 85  
DB 76 EMHTYSLHDDLP 89

RESULT 8  
US-08-886-466-2

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; Sequence 2, Application US/0886466C
; Patent No. 6040165
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohno, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/08/886,466C
; CURRENT FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; US-08-886-466-2

Query Match
Best Local Similarity 100.0%; Score 14; DB 3; Length 297;
Pred. No. 8.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 9
; US-09-475-304-2
; Sequence 2, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohno, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; CURRENT FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; US-09-475-304-2

Query Match
Best Local Similarity 100.0%; Score 14; DB 3; Length 297;
Pred. No. 8.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 10
; US-09-101-126-3
; Sequence 3, Application US/09101126
; Patent No. 6316216
; GENERAL INFORMATION:
; APPLICANT: OHNO, CHIKARA
; APPLICANT: NAKANE, HIROYUKI
```

```
; APPLICANT: NISHINO, TOKUZO
; APPLICANT: OHNUMA, SHINICHI
; APPLICANT: HIROOKA, KAZUTAKE
; TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
; FILE REFERENCE: 77670/566
; CURRENT APPLICATION NUMBER: US/09/101,126
; CURRENT FILING DATE: 1999-04-27
; EARLIER APPLICATION NUMBER: PCT/JP97/03921
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: JP 8-307506
; EARLIER FILING DATE: 1996-11-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; OTHER INFORMATION: 86-92 is an Asp-rich domain
; US-09-101-126-3

Query Match
Best Local Similarity 100.0%; Score 14; DB 4; Length 297;
Pred. No. 8.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 11
; US-09-367-528A-5
; Sequence 5, Application US/09367528A
; Patent No. 6395525
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; US-09-367-528A-5

Query Match
Best Local Similarity 100.0%; Score 14; DB 4; Length 297;
Pred. No. 8.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 12
; US-09-275-742-2
; Sequence 2, Application US/09275742
; Patent No. 6130069
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwin Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: ispa
; FILE REFERENCE: GM10205
; CURRENT APPLICATION NUMBER: US/09/275,742
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
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LENGTH: 291  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-275-742-2

Query Match 3.8%; Score 11; DB 3; Length 291;  
Best Local Similarity 100.0%; Pred. No. 0.0073;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SLIHDLPLAMD 88  
DB 76 SLIHDLPLAMD 86

RESULT 13  
US-09-217-609A-6  
Sequence 6, Application US/09217609A

GENERAL INFORMATION:  
APPLICANT: MURAMATSU Masayoshi  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OGURA, Kyoza  
APPLICANT: Koyama, Tanetoshi  
APPLICANT: SHIMIZU, Naoto  
APPLICANT: CHO, Yewwin  
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, NW - Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: US  
ZIP: 20036

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: Wordperfect 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/217,609A  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/873,235  
FILING DATE: 11-Jun-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: TOFFENETTI, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 10235/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-1776  
TELEFAX: 202-429-0796

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 320 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-217-609A-6

Query Match 3.1%; Score 9; DB 3; Length 320;  
Best Local Similarity 100.0%; Pred. No. 0.76;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 AGGKRIRPV 48  
DB 42 AGGKRIRPV 50

RESULT 14  
US-08-873-235B-6  
Sequence 6, Application US/08873235B

Patent No. 6174715  
GENERAL INFORMATION:  
APPLICANT: MURAMATSU Masayoshi  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OGURA, Kyoza  
APPLICANT: Koyama, Tanetoshi  
APPLICANT: SHIMIZU, Naoto  
APPLICANT: CHO, Yewwin  
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, NW - Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: US  
ZIP: 20036

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: Wordperfect 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/873,235B  
FILING DATE: 11-Jun-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 154441/1996  
FILING DATE: 14-Jun-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: TOFFENETTI, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 10235/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-429-1776  
TELEFAX: 202-429-0796

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 320 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-873-235B-6

Query Match 3.1%; Score 9; DB 3; Length 320;  
Best Local Similarity 100.0%; Pred. No. 0.76;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 AGGKRIRPV 48  
DB 42 AGGKRIRPV 50

RESULT 15  
US-09-328-352-5590  
Sequence 5590, Application US/09328352

GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5590  
LENGTH: 219  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5590

Query Match 2.8%; Score 8; DB 4; Length 219;  
Best Local Similarity 100.0%; Pred. No. 5.2;

Matches	8;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	7	NKLIDEVN	14						
Db	31	NKLIDEVN	38						

Search completed: November 26, 2003, 15:41:12  
Job time : 21 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:40:11 : Search time 31 Seconds  
(without alignments)  
1707.588 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 287  
Sequence: 1 MTNLPNKLIDVNNELSAVA.....ELTQIDEGNTKLLLEIVDL 287

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	287	100.0	287 10 US-09-925-637-64	Sequence 64, Appl
2	287	100.0	287 15 US-10-084-205-64	Sequence 64, Appl
3	197	68.6	293 9 US-09-815-242-12583	Sequence 12583, A
4	192	66.9	288 9 US-09-815-242-5239	Sequence 5239, AP
5	18	6.3	293 9 US-09-815-242-10630	Sequence 10630, A
6	15	5.2	297 10 US-09-934-903-14	Sequence 14, Appl
7	15	5.2	297 11 US-09-941-947A-72	Sequence 20, Appl
8	15	5.2	297 11 US-09-941-947A-72	Sequence 11239, A
9	12	4.2	295 9 US-09-815-242-11063	Sequence 10063, A
10	12	4.2	299 9 US-09-815-242-14084	Sequence 14084, A
11	12	4.2	299 9 US-09-815-242-14084	Sequence 14084, A
12	11	3.8	291 9 US-09-815-242-13273	Sequence 13273, A
13	11	3.8	291 9 US-09-815-242-13597	Sequence 13597, A
14	11	3.8	303 9 US-09-815-242-11382	Sequence 11382, A
15	11	3.8	303 9 US-09-815-242-11547	Sequence 11547, A

16	9	3.1	287 12 US-10-166-225A-159	Sequence 159, App
17	8	2.8	171 14 US-10-108-915-24	Sequence 24, Appl
18	8	2.8	226 10 US-09-981-876-145	Sequence 145, App
19	8	2.8	226 11 US-09-148-545-145	Sequence 145, App
20	8	2.8	295 9 US-09-815-242-11971	Sequence 11971, A
21	8	2.8	316 14 US-10-108-915-16	Sequence 16, Appl
22	8	2.8	316 14 US-10-108-915-20	Sequence 20, Appl
23	8	2.8	316 14 US-10-108-915-45	Sequence 45, Appl
24	8	2.8	326 14 US-10-108-915-46	Sequence 46, Appl
25	8	2.8	330 11 US-09-244-330-22	Sequence 22, Appl
26	8	2.8	330 12 US-10-066-108-39	Sequence 39, Appl
27	8	2.8	330 12 US-10-066-203-39	Sequence 39, Appl
28	8	2.8	330 12 US-10-223-081-178	Sequence 178, App
29	8	2.8	330 12 US-10-223-082-178	Sequence 178, App
30	8	2.8	330 14 US-10-066-500-39	Sequence 39, Appl
31	8	2.8	330 15 US-10-002-796-39	Sequence 39, Appl
32	8	2.8	330 15 US-10-066-273-39	Sequence 39, Appl
33	8	2.8	330 15 US-10-066-494-39	Sequence 39, Appl
34	8	2.8	330 15 US-10-066-269-39	Sequence 39, Appl
35	8	2.8	330 15 US-10-066-211-39	Sequence 39, Appl
36	8	2.8	330 15 US-10-066-193-39	Sequence 39, Appl
37	8	2.8	330 15 US-10-223-085-178	Sequence 178, App
38	8	2.8	330 15 US-10-226-739-39	Sequence 39, Appl
39	8	2.8	330 15 US-10-223-084-178	Sequence 178, App
40	8	2.8	330 15 US-10-223-088-178	Sequence 178, App
41	8	2.8	330 15 US-10-223-090-178	Sequence 178, App
42	8	2.8	330 15 US-10-223-087-178	Sequence 178, App
43	8	2.8	330 15 US-10-223-083-178	Sequence 178, App
44	8	2.8	330 15 US-10-223-089-178	Sequence 178, App
45	8	2.8	342 14 US-10-108-915-38	Sequence 38, Appl

#### ALIGNMENTS

RESULT 1  
US-09-925-637-64  
Sequence 64, Application US/09925637  
Patent No. US20020103338A1  
GENERAL INFORMATION:  
APPLICANT: Choi  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: PB560  
CURRENT APPLICATION NUMBER: US/09/925,637  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/151,933  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781,986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956,171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009,861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 64  
LENGTH: 287  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-637-64  
Query Match 100.0%; Score 287; DB 10; Length 287;  
Best Local Similarity 100.0%; Pred. No. 5.8e-270; Indels 0; Gaps 0;  
Matches 287; Conservative 0; Mismatches 0;

QY 1 MTNLPNKLIDVNNELSAVINKSWVDQLEESMLYSNAGGKRIRPVLLITLDSLNE 60  
DB 1 MTNLPNKLIDVNNELSAVINKSWVDQLEESMLYSNAGGKRIRPVLLITLDSLNE 60  
QY 61 YELGKMSALALEMIHTYSLIHDDLPMQNDVDVRRGLTNHXYGWTALADALLTKAF 120

Db 61 YELGMSAIALEMIHTYSLIHDDLPAVNDNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120  
QY 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKRTGA 180  
Db 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKRTGA 180  
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMMFQIKNDLLDCYGEBAKLGKVGSDLEN 240  
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMMFQIKNDLLDCYGEBAKLGKVGSDLEN 240  
QY 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287  
Db 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

## RESULT 2

US-10-084-205-64  
Sequence 64, Application US/10084205  
Publication No. US20030049648A1  
GENERAL INFORMATION:  
APPLICANT: Choi, Gil  
TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides  
FILE REFERENCE: P515P1  
CURRENT APPLICATION NUMBER: US/10/084,205  
CURRENT FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: 60/151,933  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 64  
LENGTH: 287  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-10-084-205-64

Query Match 100.0%; Score 287; DB 15; Length 287;  
Best Local Similarity 100.0%; Pred. No. 5.8e-270;  
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIDEVNNELSAINKSVMDTOLESMTLSNAGKRRIRPVLLLTLDLSLNT 60  
Db 1 MTNLPNNKLIDEVNNELSAINKSVMDTOLESMTLSNAGKRRIRPVLLLTLDLSLNT 60  
QY 61 YELGMSAIALEMIHTYSLIHDDLPAVNDNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120  
Db 61 YELGMSAIALEMIHTYSLIHDDLPAVNDNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120  
QY 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKRTGA 180  
Db 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKRTGA 180  
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMMFQIKNDLLDCYGEBAKLGKVGSDLEN 240  
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMMFQIKNDLLDCYGEBAKLGKVGSDLEN 240  
QY 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287  
Db 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

## RESULT 3

US-09-815-242-12583  
Sequence 12583, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12583  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-09-815-242-12583

Query Match 68.6%; Score 197; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.1e-182;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIDEVNNELSAINKSVMDTOLESMTLSNAGKRRIRPVLLLTLDLSLNT 60  
Db 1 MTNLPNNKLIDEVNNELSAINKSVMDTOLESMTLSNAGKRRIRPVLLLTLDLSLNT 60  
QY 61 YELGMSAIALEMIHTYSLIHDDLPAVNDNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120  
Db 61 YELGMSAIALEMIHTYSLIHDDLPAVNDNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120  
QY 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKRTGA 180  
Db 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKRTGA 180  
QY 181 LITFAVMSAADIANVDD 197  
Db 181 LITFAVMSAADIANVDD 197

## RESULT 4

US-09-815-242-5239  
Sequence 5239, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5239
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5239

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Query Match 66.9%; Score 192; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.7e-178;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 MNKLIDEVNNELSVAINKSYMDTQLESMTLSINAGKRIKRPVLLLTDSINTREYELGM 65
DB 1 MNKLIDEVNNELSVAINKSYMDTQLESMTLSINAGKRIKRPVLLLTDSINTREYELGM 60
QY 66 KSAIALEMITYSLIHDDLPAMDNDYRRGKLTNNKXYGEMTAIIAGDALLTAFAELISS 125
DB 61 KSAIALEMITYSLIHDDLPAMDNDYRRGKLTNNKXYGEMTAIIAGDALLTAFAELISS 120
QY 126 DDLRLTEVVKIKVLRSLASAGHVGWGMIDMQSECPIDLETLEMINKTKGALLTFA 185
DB 121 DDLRLTEVVKIKVLRSLASAGHVGWGMIDMQSECPIDLETLEMINKTKGALLTFA 180
QY 186 VMSAADIANDVD 197
DB 181 VMSAADIANDVD 192

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RESULT 5
US-09-815-242-10630
; Sequence 10630, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITPA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10630

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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10630

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Query Match 6.3%; Score 18; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 71 LEMHTYSLIHDDLPAMD 88
DB 71 LEMHTYSLIHDDLPAMD 88

```

```

RESULT 6
US-09-934-903-14

```

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; Sequence 14, Application US/09934903
; Patent No. US20020102690A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Matheos
; APPLICANT: Odem, J. Martin
; APPLICANT: Schenzle, Andreas J.
; APPLICANT: No. US20020102690A1ton, Kelley C.
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Rouviere, Pierre
; APPLICANT: Picataggio, Stephen
; APPLICANT: Cheng, Qiong
; TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
; FILE REFERENCE: CL1646 US NA
; CURRENT APPLICATION NUMBER: US/09/934,903
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: September 1, 2001
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Methylobionas 16a
; FEATURE:
; OTHER INFORMATION: Amino acid sequences encoded by ORF7
US-09-934-903-14

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Query Match 5.2%; Score 15; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 77 YSLIHDDLPAMDND 91
DB 80 YSLIHDDLPAMDND 94

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```

RESULT 7
US-09-934-868-72
; Sequence 72, Application US/09934868
; Patent No. US20020137190A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Matheos
; APPLICANT: Odem, James M
; APPLICANT: Schenzle, Andreas J
; APPLICANT: Schenzle, Andreas J
; TITLE OF INVENTION: IDENTIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFERENCE: CL1596 US NA
; CURRENT APPLICATION NUMBER: US/09/934,868
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 72
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Methylobionas 16a
; FEATURE:

```

OTHER INFORMATION: Amino acid sequences encoded by ORF7 - ISPa  
US-09-934-868-72

Query Match 5.2%; Score 15; DB 10; Length 297;  
Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMNDND 91  
Db 80 YSLIHDDLPMNDND 94

## RESULT 8

US-09-941-947A-20  
Sequence 20, Application US/09941947A  
Publication No. US2003000528A1  
GENERAL INFORMATION:  
APPLICANT: Brzostowicz, Patricia C.  
APPLICANT: Cheng, Qiong  
APPLICANT: DiCosimo, Deana J.  
APPLICANT: Koffas, Matheos  
APPLICANT: Miller, Edward S. Jr.  
APPLICANT: Odom, J. Martin  
APPLICANT: Picataggio, Steve E.  
APPLICANT: Rouviere, Pierre E.  
TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE  
FILE REFERENCE: C11903 US NA  
CURRENT APPLICATION NUMBER: US/09/941,947A  
CURRENT FILING DATE: 2001-09-01  
PRIOR APPLICATION NUMBER: 60/229,907  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,858  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 20  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Methylomonas 16a  
US-09-941-947A-20

Query Match 5.2%; Score 15; DB 11; Length 297;  
Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMNDND 91  
Db 80 YSLIHDDLPMNDND 94

## RESULT 9

US-09-815-242-11239  
Sequence 11239, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11239  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Haemophilus influenzae  
US-09-815-242-11239

Query Match 4.2%; Score 12; DB 9; Length 295;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMND 88  
Db 80 YSLIHDDLPMND 91

RESULT 10  
US-09-815-242-10069  
Sequence 10069, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10069  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-815-242-10069

Query Match 4.2%; Score 12; DB 9; Length 299;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMND 88  
Db 79 YSLIHDDLPMND 90

```

RESULT 11
US-09-815-242-14084
; Sequence 14084, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14084
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-14084

Query Match          4.2%; Score 12; DB 9; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 YSLHDDLPMAMD 88
Db      79 YSLHDDLPMAMD 90

RESULT 12
US-09-815-242-13273
; Sequence 13273, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23

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; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13273
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13273

Query Match          3.8%; Score 11; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 SLIHDDLPMAMD 88
Db      76 SLIHDDLPMAMD 86

RESULT 13
US-09-815-242-13597
; Sequence 13597, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13597
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13597

Query Match          3.8%; Score 11; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 SLIHDDLPMAMD 88
Db      76 SLIHDDLPMAMD 86

```

Db 76 SLIHHDDLPAMD 86

## RESULT 14

US-09-815-242-11382  
; Sequence 11382, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseelbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyekind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; NUMBER OF SEQ ID NOS: 1410  
; SEQ ID NO 11382  
; LENGTH: 303  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori  
US-09-815-242-11382

## Query Match

3.8%; Score 11; DB 9; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHHDDLP 85

Db 85 HTYSLIHHDDLP 95

## RESULT 15

US-09-815-242-11547  
; Sequence 11547, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseelbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyekind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 1410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11547  
; LENGTH: 303  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori  
US-09-815-242-11547

## Query Match

3.8%; Score 11; DB 9; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHHDDLP 85

Db 85 HTYSLIHHDDLP 95

Search completed: November 26, 2003, 15:45:38  
Job time : 31 secs



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QY 41 G|YGL|YLYSARGL|EARGP|ROVAL|LEULEULEUTH|LEUASP|SER|LEUA|ENTH|GLU 60
DB 121 GGAGST|AAAGCAT|CCAGCAT|GTTCT|GTTAT|TACT|CTT|AGAT|CACT|AAAT|ACCGAG 180
QY 61 TYR|GLU|LEU|GLY|MET|LYS|SER|A|A|I|E|A|LEU|GLU|MET|I|EH|S|TH|TYR|SER|LEU|I|E 80
DB 181 TAT|GAT|T|AG|G|T|G|T|G|A|A|G|G|G|C|A|A|T|T|G|C|A|T|A|A|A|T|G|A|T|T|C|A|T|A|T|T|C|T|A|T|T 240
QY 81 H|I|E|A|S|P|S|E|P|P|RO|A|I|A|MET|E|S|E|A|A|A|S|P|S|Y|R|A|R|G|L|Y|L|E|U|T|H|A|S|N|H|I|S 100
DB 241 CAT|GAT|AT|C|T|A|C|C|A|G|G|A|G|G|A|T|G|A|T|G|A|T|A|T|G|A|G|A|G|A|A|T|T|A|A|C|A|A|T|CAT 300
QY 101 L|Y|E|V|A|L|TYR|G|L|Y|U|T|P|T|H|R|A|A|I|E|L|E|U|A|A|G|L|Y|A|S|P|A|I|A|LEU|LEU|T|H|R|Y|S|A|I|P|H|E 120
DB 301 A|A|A|G|T|A|T|G|T|G|A|T|G|G|A|C|T|G|C|A|T|A|T|T|A|G|C|A|G|T|A|T|G|C|T|T|A|T|T|A|A|A|G|C|A|T|T 360
QY 121 G|L|U|L|E|U|I|E|S|E|S|E|A|S|P|A|S|P|A|R|G|L|E|U|T|H|A|S|P|G|L|U|V|A|L|Y|S|I|E|L|Y|S|V|A|L|LEU|G|I|N|A|R|G 140
DB 361 G|A|A|C|T|A|T|T|T|C|A|A|G|T|G|A|T|G|A|T|A|C|T|G|A|T|G|A|T|A|A|A|A|A|A|G|T|T|C|T|A|C|A|A|C|G|G 420
QY 141 L|E|U|S|E|R|I|E|A|S|E|R|G|L|Y|H|I|S|V|A|L|G|L|Y|E|V|A|L|G|L|Y|G|I|N|E|T|L|E|U|A|S|P|M|E|T|G|I|N|S|E|R 160
DB 421 C|T|G|C|A|A|T|A|G|C|A|A|G|T|G|C|A|T|G|T|G|G|A|T|G|G|T|C|G|C|G|C|A|A|A|G|T|A|G|A|T|G|C|A|A|A|G|C 480
QY 161 G|L|U|G|L|Y|G|I|N|P|R|O|I|L|E|A|S|P|L|E|U|G|L|U|T|H|L|E|U|G|L|U|E|T|I|E|H|S|L|Y|S|T|H|R|Y|S|T|H|G|L|Y|A| 180
DB 481 G|A|A|G|G|C|C|A|C|A|A|T|T|G|A|T|T|T|G|A|A|C|T|T|G|A|A|T|G|A|T|A|C|A|A|A|A|A|A|A|A|G|G|A|G|C|A 540
QY 181 L|E|U|L|E|U|T|H|R|P|H|E|A|V|A|L|E|T|S|E|R|A|A|I|A|S|P|I|E|A|S|N|V|A|L|A|S|P|A|R|T|H|R|Y|S 200
DB 541 T|T|A|T|T|A|C|T|T|T|G|G|T|T|A|G|A|T|G|G|A|G|C|A|G|A|T|G|C|T|A|T|G|C|A|T|G|A|T|G|C|A|A|C|T|T|A|A 600
QY 201 G|L|U|H|I|S|E|U|G|L|U|S|E|R|T|Y|R|H|I|S|L|E|U|G|L|Y|E|U|E|T|P|H|E|G|I|N|I|E|L|Y|S|A|S|P|L|E|U 220
DB 601 G|A|A|C|A|T|T|A|A|A|A|G|T|T|A|G|T|T|A|C|A|T|T|A|G|T|A|G|T|A|G|T|T|C|A|G|A|T|T|A|A|A|G|A|T|T|A 660
QY 221 L|E|U|A|S|P|C|Y|E|T|Y|R|G|L|Y|A|S|P|G|L|U|A|L|Y|S|E|U|G|L|Y|S|E|V|A|L|G|L|Y|S|E|R|A|S|P|L|E|U|A|S|N 240
DB 661 T|T|A|G|C|T|A|T|G|T|G|T|A|G|A|G|C|A|A|A|G|T|T|A|G|T|A|A|A|A|A|G|G|G|C|A|C|G|C|A|C|T|T|G|A|A|A|T 720
QY 241 A|S|N|L|Y|S|E|R|T|H|R|Y|V|A|L|S|E|R|L|E|U|G|L|Y|S|A|S|P|G|L|Y|A|G|L|U|A|S|P|L|Y|S|L|E|U|T|H|R|Y|S 260
DB 721 A|A|T|T|A|A|A|G|T|A|C|G|T|A|C|G|A|T|T|A|T|T|A|G|G|A|A|A|G|T|G|C|C|A|G|A|A|T|T|A|A|T|T|G|A|C|T|T|A|T 780
QY 261 H|I|S|A|R|G|A|S|P|A|A|A|V|A|L|A|S|P|G|L|U|L|E|U|T|H|G|I|N|I|E|A|S|P|G|L|U|G|I|N|P|H|E|A|S|N|T|H|R|Y|S|H|I|S 280
DB 781 C|A|T|A|G|A|G|A|C|C|A|G|A|G|G|A|G|A|T|G|A|A|C|T|A|A|C|C|A|A|T|T|G|A|T|G|A|C|A|A|T|T|C|A|A|T|A|C|A|A|A|C|A|C 840
QY 281 L|E|U|L|E|U|G|L|U|L|E|V|A|L|A|S|P|L|E|U 287
DB 841 T|T|A|T|T|A|G|A|A|T|C|G|T|T|G|A|T|T|A 861

RESULT 2
US-09-134-001C-334
; Sequence 334, Application US/09134001C
; Patient No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 334
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
```

```
US-09-134-001C-334
Alignment Scores:
Pred. No.: 1,81e-115 Length: 909
Score: 1015.00 Matches: 197
Percent Similarity: 82.93% Conserves: 41
Best Local Similarity: 68.64% Mismatches: 49
Query Match: 69.86% Indels: 0
DB: 4 Gaps: 0

US-09-925-637-64 (1-287) x US-09-134-001C-334 (1-909)
QY 1 Met|Th|Asn|Leu|Pro|Met|Asn|Lys|Leu|Leu|Asp|Glu|Val|Asn|Asn|Glu|Leu|Ser|Val|A|A| 20
DB 28 ATG|AAG|AACT|A|C|A|G|T|G|A|T|A|T|A|T|A|A|A|T|A|A|T|A|A|T|A|A|T|A|C|A|C|A|C|G|A|T|A|A|G|T|C|A 87
QY 21 L|I|E|A|S|N|L|Y|S|E|R|V|A|L|E|T|A|S|P|T|H|R|G|I|N|L|E|U|G|L|U|S|E|R|M|E|T|L|E|U|T|Y|R|S|E|R|L|E|U|A|N|A| 40
DB 88 A|T|A|C|A|A|T|C|A|C|A|C|A|T|T|A|A|A|A|C|T|A|T|T|A|G|A|A|G|A|A|G|A|T|G|A|A|A|T|T|C|A|T|T|A|A|A|T|G|C|T 147
QY 41 G|L|Y|G|L|Y|L|E|A|R|G|P|RO|V|A|L|L|E|U|L|E|U|T|H|L|E|U|A|S|P|S|E|R|L|E|U|A|S|N|T|H|R|Y|S| 60
DB 148 G|G|G|T|P|A|A|A|A|G|A|T|G|A|C|C|A|G|C|A|T|A|T|T|A|T|T|A|C|A|C|T|A|A|A|A|A|T|G|C|T|T|A|C|A|A|A|G|A|T 207
QY 61 TYR|GLU|LEU|GLY|MET|LYS|SER|A|A|I|E|A|LEU|GLU|MET|I|EH|S|TH|TYR|SER|LEU|I|E 80
DB 208 T|A|T|C|A|C|A|A|G|A|C|T|A|A|A|T|G|C|T|T|A|G|C|A|T|T|G|A|A|A|T|G|A|T|T|C|A|T|A|T|T|C|T|T|A|T|T 267
QY 81 H|I|E|A|S|P|S|E|P|P|RO|A|I|A|MET|E|S|E|A|A|A|S|P|S|Y|R|A|R|G|L|Y|L|E|U|T|H|A|S|N|H|I|S 100
DB 268 C|A|T|G|A|T|A|T|T|A|C|C|A|C|A|A|T|G|A|T|G|A|T|G|A|C|G|A|T|T|A|C|C|T|A|G|A|G|A|A|A|T|T|A|C|A|A|A|T|C|A|T 327
QY 101 L|Y|E|V|A|L|TYR|G|L|Y|U|T|P|T|H|R|A|A|I|E|L|E|U|A|A|G|L|Y|A|S|P|A|I|E|U|L|E|U|T|H|R|Y|S|A|I|P|H|E 120
DB 328 A|A|G|T|T|A|T|G|G|A|A|G|A|A|G|C|A|T|T|C|T|G|G|G|A|G|C|A|T|T|A|T|T|A|C|A|A|A|G|C|T|T|T 387
QY 121 G|L|U|L|E|U|I|E|S|E|S|E|A|S|P|A|S|P|A|R|G|L|E|U|T|H|A|S|P|G|L|U|V|A|L|Y|S|I|E|L|Y|S|V|A|L|LEU|G|I|N|A|R|G 140
DB 388 G|A|A|T|G|T|T|C|T|A|T|A|T|A|C|T|A|C|A|T|T|G|A|A|G|A|T|G|T|G|A|A|A|G|T|A|T|T|A|A|A|A|A|G|A 447
QY 141 L|E|U|S|E|R|I|E|A|S|E|R|G|L|Y|H|I|S|V|A|L|G|L|Y|E|V|A|L|G|L|Y|G|I|N|E|T|L|E|U|A|S|P|M|E|T|G|I|N|S|E|R 160
DB 448 C|T|T|T|C|A|A|A|G|C|A|A|G|T|G|C|A|T|T|G|G|A|A|G|T|G|G|G|G|C|C|A|A|G|C|C|T|T|G|A|T|G|A|A|G|T 507
QY 161 G|L|U|G|L|Y|G|I|N|P|R|O|I|L|E|A|S|P|L|E|U|G|L|U|T|H|L|E|U|G|L|U|E|T|I|E|H|S|L|Y|S|T|H|R|Y|S|T|H|G|L|Y|A| 180
DB 508 G|A|A|G|G|A|A|G|C|A|A|T|T|G|T|T|A|G|A|C|T|T|A|G|A|T|C|A|A|T|T|C|A|T|G|A|A|C|T|A|A|G|A|C|A|G|C|G|C|T 567
QY 181 L|E|U|L|E|U|T|H|R|P|H|E|A|V|A|L|E|T|S|E|R|A|A|I|A|S|P|I|E|A|S|N|V|A|L|A|S|P|A|R|T|H|R|Y|S 200
DB 568 T|T|A|C|T|A|A|T|T|T|C|A|G|T|A|T|G|C|G|G|T|A|G|C|A|T|T|G|C|C|A|G|T|G|C|C|A|G|T|A|G|A|C|A|A|A|T|A|T|T|G|C|T 627
QY 201 G|L|U|H|I|S|E|U|G|L|U|S|E|R|T|Y|R|H|I|S|L|E|U|G|L|Y|E|U|E|T|P|H|E|G|I|N|I|E|L|Y|S|A|S|P|L|E|U 220
DB 628 A|A|G|A|A|T|T|A|G|A|A|A|T|T|A|G|T|C|A|T|T|A|G|G|A|T|A|T|G|T|T|C|A|A|T|T|A|A|A|G|T|T|A 687
QY 221 L|E|U|A|S|P|C|Y|E|T|Y|R|G|L|Y|A|S|P|G|L|U|A|L|Y|S|E|U|G|L|Y|S|E|V|A|L|G|L|Y|S|E|R|A|S|P|L|E|U|A|S|N 240
DB 688 C|T|G|A|G|G|T|A|T|G|T|A|G|T|A|T|A|A|A|C|T|T|G|C|A|A|A|A|A|A|G|T|G|G|C|G|A|T|A|T|A|G|A|A|T 747
QY 241 A|S|N|L|Y|S|E|R|T|H|R|Y|V|A|L|S|E|R|L|E|U|G|L|Y|S|A|S|P|G|L|Y|A|G|L|U|A|S|P|L|Y|S|L|E|U|T|H|R|Y|S 260
DB 748 C|A|T|A|A|A|G|T|A|T|T|A|T|T|C|T|T|A|C|T|T|G|A|A|A|A|A|G|G|A|G|C|A|G|A|A|A|A|G|T|T|A|A|C|A|A|T 807
QY 261 H|I|S|A|R|G|A|S|P|A|A|A|V|A|L|A|S|P|G|L|U|L|E|U|T|H|G|I|N|I|E|A|S|P|G|L|U|G|I|N|P|H|E|A|S|N|T|H|R|Y|S|H|I|S 280
DB 808 C|A|T|C|A|A|T|A|T|C|T|G|C|T|A|G|A|G|C|T|T|A|A|T|T|G|A|A|A|T|T|G|A|C|A|A|A|T|T|G|A|C|A|A|A|T|A|T|G|A|T|C|T|G|A|A 867
QY 281 L|E|U|L|E|U|G|L|U|L|E|V|A|L|A|S|P|L|E|U 287
DB 868 T|T|A|A|G|T|A|T|T|G|T|A|G|A|T|T|A 888

RESULT 3
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US-08-534-910B-4  
Sequence 4, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOTAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Tofteneft, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)428-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 894 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-4  
Alignment Scores:  
Pred. No.: 1.85e-71 Length: 894  
Score: 657.00 Matches: 133  
Percent Similarity: 68.10% Conservative: 57  
Best Local Similarity: 47.67% Mismatches: 83  
Query Match: 45.22% Indels: 6  
Gaps: 2  
US-09-925-637-64 (1-287) x US-08-534-910B-4 (1-894)  
QY 1 MetThrasnleuPromeLanlybLeuIlleAspGluValAsnAngluLeuSerValAla 20  
DB 1 ATGGCGAGCTTTCAGTTGAACGATTCTCAACGACGAAAAACAGGCGGTGAACAGCG 60  
QY 21 IleAsnlySerValMet-----AspThrGlnLeuGluGluGluSerMetLeuTyr 36  
DB 61 CTCCTCCGTTATATAGAGCGCTTAGAGGCGCGCGGAGCTGAAAAAGCGATGGCTTAC 120  
QY 37 SerLeuAsnAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 56  
DB 121 TCATTGGAGGCGCGCGCGGCAACGATCCGTCGTTGCTGCTTCACCGTTGGGCG 180

QY 57 LeuAsnThrGlnTyrGlnLeuGluGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76  
DB 181 CTCGGCAAGACCGCGCGCGGTGCGATTCGCCGCTGCGCATTAATGATTCATACG 240  
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96  
DB 241 CACTCTTATCATCATGATGATTTGGCCGACATGCAACAGATGATTTGGCGCGCGCAAG 300  
QY 97 LeuThrAsnHisLysValTyrGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 116  
DB 301 CCACGCAACCATTAAGTGTTCGCGGAGCGGCGGATGCGCATTTGCGGCGGAGCGGTTG 360  
QY 117 ThrLysAlaPheGluLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134  
DB 361 ACCTACGCTTTCATATTGATTCACCGAATCGACGATGACGATGATCCCTCTCCGCGG 420  
QY 135 IleLysValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154  
DB 421 CTTCGCTCATCGAAGCGCTGGGAAAGCGCGCGCTCCGAAAGGATGATCGCGGCTCAG 480  
QY 155 MetLeuAspMetGlnSerGlnGlnProIleAspLeuGluThrLeuGluMetIleHis 174  
DB 481 GCAGCGCATATGAT 540  
QY 175 LysThrLysThrGlyValAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAla 194  
DB 541 CGGATTAACCGGGAAGAAATGCTGCAATACAGGCTCAGCGCGCGCTTGAATCGCGCG 600  
QY 195 ValAspAspThrThrLysGlnHisLysLeuSerTyrSerTyrHisLysLeuMetCp 214  
DB 601 GGTGATGCCCGGAAACGCGGAGCTTGAAGATTCGCGCGCATTCAGGCTTGCCTT 660  
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysVal 234  
DB 661 CAATTCGCGATGATATTCATGATTTGAAGGCGGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 235 GlySerAspLeuGlnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254  
DB 721 GCGAGCGACCAACGACCAACGACGATTCAGCGCTTGTCTGCTGCGTCCGCGCGCG 780  
QY 255 GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273  
DB 781 AAGAAAGATTGACGTTTCATATCGAGGCGCGGCGCATTTACGAAAGCGCGAC 837  
RESULT 4  
US-08-534-910B-5  
Sequence 5, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOTAMA, Tanetoshi  
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B

FILING DATE: 28-SEP-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-25253  
 FILING DATE: 14-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Toffenetti, Judith L.  
 REGISTRATION NUMBER: 39,048  
 REFERENCE/DOCKET NUMBER: 77670/398  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 429-1776  
 TELEFAX: (202) 429-0796  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 894 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus stearothermophilus*  
 US-08-534-910B-5

Alignment Scores:  
 Pred. No.: 2,45e-71 Length: 894  
 Score: 656.00 Matches: 133  
 Percent Similarity: 67.38% Conservative: 55  
 Best Local Similarity: 47.67% Mismatches: 85  
 Query Match: 45.15% Indels: 6  
 DB: 1 Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-5 (1-894)

Qy 1 MetthrleuPromeAenlyLeuileaspGluValaenagluLeuSerVala 20  
 Db 1 ATGGCGAGCTTTCAGTTGAAACAGTTCTCAACGAGCAAAACAGCGGAGAAACAGCG 60  
 Qy 21 IleasnlySerValmet-----AspThrGluLeuGluGluSerMetLeuTyr 36  
 Db 61 CTCCTCCGTTATATAGACCGCTTGAAAGCGCGCGCAAGCTGAAAGGCGATGCGCTAC 120  
 Qy 37 SerleuanaIaglylyysargilearProValleuLeuLeuLeuThrLeuaspSer 56  
 Db 121 TCATTGAGGCGCGCGCAACGAAATCGTCCGTTGCTGCTGCTCACCGTTCAAGCG 180  
 Qy 57 LeuasnThrGluTyrGluLeuGlyMetlySerAlaIlealeuGluMetIleHisThr 76  
 Db 181 CTCGCGAAAGACCGCGCGCTCGATTCGCCCTCGCGGATGAAATGATCCATACG 240  
 Qy 77 TySerleuIleHisaspPleuProAlaMetaspAnaaspPyrTatGATGlylys 96  
 Db 241 TACTCTTGTATCATGATGATTTGCCAGCATGACAACTGATTTGCCGCGCGCAAG 300  
 Qy 97 LeuThrAnhislyValTyrGlyGluTyrThrAlaIleleuIaglyaspAlaLeuLeu 116  
 Db 301 CCGACGAACATAAAGTTCGCGGAGCGATGCGCATCTTGGCGGGAGCGGTTGTTG 360  
 Qy 117 ThrlyAlaPhegluleuIleSer-----SerAspAspArgleuThrAspGluVallys 134  
 Db 361 ACGTACCGCTTCAATGATCAACGAAATCGACGATGAGCGCATCCCTCCGCTCGCG 420  
 Qy 135 IlelyValleuGluIleuGluSerIleAlaSerGlyHisValaIleGlyMetValaGlyGln 154  
 Db 421 CTTCGCTCTTCGAACGCGCTGCGCAAGCGCGCTCGGAGGAGATGTTGCCGCTCAG 480  
 Qy 155 MetleuaspMetGlnserGluGluGlnProIleaspLeuGluThrLeuGluMetIleHis 174  
 Db 481 GCAGCGCATATGGAAGAGAGGGAAGAAACGCTTTCGAGCGCTCGAATACATTCAT 540  
 Qy 175 LysThrlyThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleaspIleAlaasn 194  
 Db 541 CCGCATAAACCGGGAATAATGCTGCATATACAGCGTGCACCGCGCGCTTATCGCGCGC 600

Qy 195 ValaspAspThrThrlyserGluHisleuGluSerTyrSerTyrHisleuGlyMetPhe 214  
 Db 601 GCTGATGCCCGGCAACCGCGGAGCTTGACGATTCGCCGCCCATCTAGGCTTGCTT 660  
 Qy 215 GlnIlelyaspAspLeuLeuaspCysTyrGlyaspGluAlaIleleuGlylyVal 234  
 Db 661 CAATTCCGATGATATCTCGATATTGAAGGCGCAGAGAAAAATCCGCAAGCGCGTC 720  
 Qy 235 GlySerAspLeuGluLeuasnlySerThrTyrValSerleuGluGlylyaspGlyAla 254  
 Db 721 GGCAGGACCAACCAACCAACGACGATATCCAGCTTGCTGCTGCTGCGCGGCGC 780  
 Qy 255 GluaspLyseuThrTyrHisArgaspAlaAlaValaspGluLeuThrGlnIleasp 273  
 Db 781 AAGGAAAGTTGGCGTTCCATATCGAGGCGCGCGCCGATTTAGGAAGCGCGAC 837

RESULT 5  
 US-08-333-321-1  
 Sequence 1, Application US/08333321  
 Patent No. 5786192  
 GENERAL INFORMATION:  
 APPLICANT: Obata, Shusei  
 TITLE OF INVENTION: FARNESYL PYROPHOSPHATE SYNTHETASE  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Edward W. Greason, Esq.  
 STREET: 1 Broadway  
 CITY: New York  
 STATE: N.Y.  
 COUNTRY: U.S.A.  
 ZIP: 10004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: No. 5786192epd, windows 3.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/333,321  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/953,424  
 FILING DATE: 29-SEP-1992  
 APPLICATION NUMBER: JP 3-253788  
 FILING DATE: 01-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Greason, Edward W.  
 REGISTRATION NUMBER: 18,918  
 REFERENCE/DOCKET NUMBER: 077670/00310  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 425-5288  
 TELEFAX: (212) 425-7200  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 893 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: *Bacillus stearothermophilus*  
 US-08-333-321-1  
 Alignment Scores:  
 Pred. No.: 4.31e-71 Length: 893  
 Score: 654.00 Matches: 133  
 Percent Similarity: 67.38% Conservative: 55  
 Best Local Similarity: 47.67% Mismatches: 85  
 Query Match: 45.01% Indels: 6  
 DB: 1 Gaps: 2  
 US-09-925-637-64 (1-287) x US-08-333-321-1 (1-893)

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QY 1 MetThrAsnLeuPromeAenLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGGCCGAGCTTTCAGTTGAACAGTTTCTCAACGACGAAAAACAGCGGTGGAACAGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGluLeuGluGluSerMetLeuTyr 36
DB 61 CTCCTCCGTTATATAGAGCCCTTAGAAGGCGCGGCGGACGTAAGGCGGATGGGTAC 120
QY 37 SerLeuAsnAlaGlyGlyArgGlyLeaArgProValLeuLeuLeuLeuThrLeuAspSer 56
DB 121 TCATTGGAGGCGCGCGGCAACGATCCGTCCTGCTGCTCTGTCACCGCTTCCGGCGG 180
QY 57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76
DB 181 CTCGGCAAGACCGCGCGGTGGATTTGCCGTGCGCGCGGATTTGAAATGATCCATACG 240
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
DB 241 TACTCTTGTATCATGATGATTTGCCGACGATGACACATGATTTGCCGCGCGCAAG 300
QY 97 LeuThrAsnHisLysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeu 116
DB 301 CCGACCAACCAATAAGTTTCGGAGCGATGCGCATCTTGGCGGAGCGGTTGTTG 360
QY 117 ThrLysAlaPheGluLeuLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134
DB 361 ACCTAGCGCTTTCATTTGATCACCAGAAATGACAGATGACGCGCATCTCTCTCCGTCGG 420
QY 135 IleLysValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
DB 421 CTTCGGCTCATCGAAGCGGTGGGAAAGCGCGCGGTCCGGAAGGATGTCGCGCGTCAAG 480
QY 155 MetLeuAspMetLeuSerGluGlnProIleAspLeuGluThrLeuGluMetIleHis 174
DB 481 GCAGCGCATATGAGAGAGAGGAGGAGAAACGCTACCGTTTCGAGATCGAATCATTCAT 540
QY 175 LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAla 194
DB 541 CGGCATTAACCCGGGAAAAATGCTGCATATACAGCGTGCACCGCGCTTGAATCGCGCGC 600
QY 195 ValAspAspThrThrLysGluHisLeuGluSerTyrSerTyrHisLeuGluMetPhe 214
DB 601 GGTGATGCCCGGCAACCGCGGAGCTTGAAGATTCGCGCGCATCTAGCGCTTGCCTTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysVal 234
DB 661 CAATTCGCGATATATTTCTCGATATTTGAAAGGCGGCAAGAAAAATCGCGCAAGCGGTC 720
QY 235 GlySerAspLeuGluAsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
DB 721 GGACGAGCAACCAAGCAACCAAGCAAGCATATCCAGCGTGTCTGCTGCGTTCGCGCGCG 780
QY 255 GlyAspLysLeuThrTyrHisArgAspAlaAlaValAspLeuLeuThrGlnIleAsp 273
DB 781 AAGGAAAGTTGGCGTTCCATATCGAGCGCGCGCAAGCCATTATGAGAAACGCGCAC 837

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RESULT 6  
US-08-534-910B-2

Sequence 2, Application US/08534910B  
Patent No. 5766911

GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoze  
APPLICANT: KOYAMA, Tanetsoshi  
TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl-diphosphate And Gene Coding Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon

```

STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tofenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-0796
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-2
Alignment Scores:
Pred. No.: 5,73e-71 Length: 894
Score: 653.00 Matches: 132
Percent Similarity: 67.388 Conservative: 56
Best Local Similarity: 47.318 Mismatches: 85
Query Match: 44.948 Indels: 6
DB: 1 Gaps: 2
US-09-925-637-64 (1-287) x US-08-534-910B-2 (1-894)
QY 1 MetThrAsnLeuPromeAenLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20
DB 1 ATGGCCGAGCTTTCAGTTGAACAGTTTCTCAACGACGAAAAACAGCGGTGGAACAGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGluLeuGluGluSerMetLeuTyr 36
DB 61 CTCCTCCGTTATATAGAGCCCTTAGAAGGCGCGGCGGACGTAAGGCGGATGGGTAC 120
QY 37 SerLeuAsnAlaGlyGlyArgGlyLeaArgProValLeuLeuLeuLeuThrLeuAspSer 56
DB 121 TCATTGGAGGCGCGCGGCAACGATCCGTCCTGCTGCTCTGTCACCGCTTCCGGCGG 180
QY 57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76
DB 181 CTCGGCAAGACCGCGCGGTGGATTTGCCGTGCGCGCGGATTTGAAATGATCCATACG 240
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
DB 241 TACTCTTGTATCATGATGATTTGCCGACGATGACACATGATTTGCCGCGCGCAAG 300
QY 97 LeuThrAsnHisLysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeu 116
DB 301 CCGACCAACCAATAAGTTTCGGAGCGATGCGCATCTTGGCGGAGCGGTTGTTG 360
QY 117 ThrLysAlaPheGluLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134
DB 361 ACCTAGCGCTTTCATTTGATCACCAGAAATGACAGATGACGCGCATCTCTCTCCGTCGG 420

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QY 135 IlelyValleuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
D 421 CTTGGGCTCATGAAAGCGCTGCGAAAGCGCGCTCGAAGGAGATGTCGCCGCTAG 480
QY 155 MetLeuAspMetGlnSerGlyGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
D 481 GCAGCCCATATGGAAGAGAGGAGAAACGCTGACGCTTCGAGCTCGAATACATTCAT 540
QY 175 LysThrThrThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsn 194
D 541 CGGATATTAACCGGAAAAATCTCATACGCTGACGCGCGCGCTGATCGCGGC 600
QY 195 ValAspAspThrThrLysGlnHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPhe 214
D 601 GCTGATCCCGCGCAAGCGCGGAGCTTACGCAATTCGCGCGCATTCAGGCTTGCCCTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysVal 234
D 661 CAATTCGCGATGATATTCGATATTTGAAGGCGCAAGAAATCGCGACCGCTC 720
QY 235 GlySerAspLeuGlnAsnAsnLysSerThrTyrValSerLeuGlnGlyLysAspGlyAla 254
D 721 GCGACGACCAAGCAACAAACAAAGCGACGATATCAGCGTTGCTGCTGCGCGCGC 780
QY 255 GlnAspLysLeuThrTyrHisArgAspAlaAlaValAspGlnLeuThrGlnIleAsp 273
D 781 AAGGAAAGTTGGCTTCATATCGAGGCGCGCGCATTTACGGAACCGCGAC 837

```

## RESULT 7

US-08-534-910B-3  
Sequence 3, Application US/08534910B  
Patent No. 5766911

## GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoze  
APPLICANT: Koyama, Taneosshi  
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranyl diphosphate And Gene Coding Ther  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Toffenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 429-1776  
TELEFAX: (202) 429-0796  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 894 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-3

## Alignment Scores:

Pred. No.:	1,34e-70	Length:	894
Score:	650.00	Matches:	132
Percent Similarity:	67.03%	Conservative:	55
Best Local Similarity:	47.31%	Mismatches:	86
Query Match:	44.74%	Indels:	6
DB:	1	Gaps:	2

US-09-925-637-64 (1-287) x US-08-534-910B-3 (1-894)

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QY 1 MetThrAsnLeuProMetAsnLysLeuIleAspGlnValAsnAsnGlnLeuSerValAla 20
D 1 ATGGCGAGCTTCAGTTGAAAGTTTCTCAACGACAAACAGGCGCGGAAACAGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGlnLeuGlnGlnSerMetLeuTyr 36
D 61 CTCTCCGTTATATGAGCGCTTAGAAGGCGCGCGCAAGCTGAAAAAGCGATGCGCTAC 120
QY 37 SerLeuAsnAlaGlyGlyLysArgIleArgProValLeuLeuLeuThrLeuAspSer 56
D 121 TCATTGGAGCGCGCGGCAACAAATCCGTCCTGCTGCTTCTGTCACCGCTTGGCGG 180
QY 57 LeuAsnThrGlnTyrGlnLeuGlnMetLysSerAlaIleAlaLeuGlnMetIleHisThr 76
D 181 CTCGAAAGAACCGCGCGCGCGATGCGCGCTGCGCGCGCGATGAAATGATCCATACG 240
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
D 241 TACTCTTGTATCCATATGATGATTTGCGAGCATGAGAACATCATATTTGCGCGCGCAG 300
QY 97 LeuThrAsnHisLysValTyrGlyGlnTyrThrAlaIleLeuAlaGlyAspAlaLeu 116
D 301 CCGACGAAACCATTAAGTGTTCGCGAGCGCATGCGCATCTTGCGCGGAGCGGCTTGG 360
QY 117 ThrLysAlaPheGlnLeuIleSer-----SerAspAspArgLeuThrAspGlnValLys 134
D 361 ACGTACGCGCTTCATATGATCACGAATGACGATGAGGCGATCCCTCTCGTCCGCG 420
QY 135 IlelyValleuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
D 421 CTTGGGCTCATGAAAGCGCTGCGAAAGCGCGCTCGAAGGAGATGTCGCCGCTAG 480
QY 155 MetLeuAspMetGlnSerGlyGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
D 481 GCAGCCCATATGGAAGAGAGGAGAAACGCTGACGCTTCGAGCTCGAATACATTCAT 540
QY 175 LysThrThrThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsn 194
D 541 CGGATATTAACCGGAAAAATCTCATACGCTGACGCGCGCGCTGATCGCGGC 600
QY 195 ValAspAspThrThrLysGlnHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPhe 214
D 601 GCTGATCCCGCGCAAGCGCGGAGCTTACGCAATTCGCGCGCATTCAGGCTTGCCCTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysVal 234
D 661 CAATTCGCGATGATATTCGATATTTGAAGGCGCAAGAAATCGCGACCGCTC 720
QY 235 GlySerAspLeuGlnAsnAsnLysSerThrTyrValSerLeuGlnGlyLysAspGlyAla 254
D 721 GCGACGACCAAGCAACAAACAAAGCGACGATATCAGCGTTGCTGCTGCGCGCGC 780
QY 255 GlnAspLysLeuThrTyrHisArgAspAlaAlaValAspGlnLeuThrGlnIleAsp 273
D 781 AAGGAAAGTTGGCTTCATATCGAGGCGCGCGCATTTACGGAACCGCGAC 837

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```

RESULT 8
US-08-886-466-1
; Sequence 1, Application US/08886466C
; Patent No. 6040165
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohno, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/08/886,466C
; EARLIER FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 8-191635
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
US-08-886-466-1

Alignment Scores:
Pred. No.: 1,34e-70 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: 3 Gaps: 1

US-09-925-637-64 (1-287) x US-08-886-466-1 (1-894)
QY 6 MetAsnLysLeuLeuLeuLeuValAsnAsnGluLeuSerValAlaLeuLysSerVal 25
DB 28 CTCACACGAGCAAAAACAGCGCGGTGGAACAGCGCTCCCGTATATAGACCGCTTAGAA 87
QY 26 MetAspThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAlaGlyLysArgIle 45
DB 88 GGGCGCGCGAAGCTGAAAGAGCGATGCGTACTGATGAGCGCGGCAAAACGATC 147
QY 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluLeuGlyMet 65
DB 148 CGTCCGCTGCTGCTTGTCTCCACCGCTCGGCGCTCGCAAGACCGCGCGTCCGATTG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuLysHisAspAspLeuPro 85
DB 208 CCCGTCGCTCGCGATGAAATGATCATACGACTCTTGATCCATGATGATTGCGG 267
QY 86 AlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGluGlu 105
DB 268 AGCATGAGCAACATGATTTGCGCGCGGCAAGCGAGCAACCATTAAGTGTTCGGGAG 327
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuSer--- 124
DB 328 GCGATGCGCATCTTGGCGGGGAGCGGTTTGAACGATTCACGTTTCAATTGATCACCGAA 367
QY 125 ---SerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnAlaGluSerIle 143
DB 388 ATGACACATGAGCGCATCTCTCCGTCGCGCTTCGCTCATCGAACCGCTGCGCAAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSerGluGln 163
DB 448 GCGCGCGCTCCGAAAGGATGTCGCGGTCAGGACCGCAATATGAGAGAGAGGAGAAA 507
QY 164 ProIleAspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThr 183
DB 508 ACCGTGACGCTTCCGAGCTCGAATATCATTCGCGATTAACCGGAGAAAATGCTCGCA 567

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QY 184 PheAlaValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203
DB 568 TACAGCGTCAGACCGCGCGCTTGAATCGCGCGGTGATGCGCGCAACCGCGGACCTT 627
QY 204 GluSerTyrSerTyrHisLeuGluMetMetPheGlnIleLysAspAspLeuAspCys 223
DB 628 GACGAATTCGCGCGCATCTAGGCTTGCCTTCAATTGCGCATGATATTCGATATT 687
QY 224 TyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsnAsnLysSer 243
DB 688 GAGGGCGCAAGCAAAAATCGGCAAGCCGTCGCGAGCGAACCAAGCAACAAAGCG 747
QY 244 ThrTyrValSerLeuGluGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263
DB 748 ACGATTCACAGCGTGTGTCGCTTCCGCGCGCGCAAGAGAAAGTTGGCGTTTCATCGAG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
DB 808 CGCGCGCAGCGCATTTACGGAACGCGCGAC 837

RESULT 9
US-09-475-304-1
; Sequence 1, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohno, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; EARLIER FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
US-09-475-304-1

Alignment Scores:
Pred. No.: 1,34e-70 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: 3 Gaps: 1

US-09-925-637-64 (1-287) x US-09-475-304-1 (1-894)
QY 6 MetAsnLysLeuLeuLeuValAsnAsnGluLeuSerValAlaLeuLysSerVal 25
DB 28 CTCACACGAGCAAAAACAGCGCGGTGGAACAGCGCTCCCGTATATAGACCGCTTAGAA 87
QY 26 MetAspThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAlaGlyLysArgIle 45
DB 88 GGGCGCGCGAAGCTGAAAGAGCGATGCGTACTGATGAGCGCGGCAAAACGATC 147
QY 46 ArgProValLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGluLeuGlyMet 65
DB 148 CGTCCGCTGCTGCTTGTCTCCACCGCTCGGCGCTCGCAAGACCGCGCGTCCGATTG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuLysHisAspAspLeuPro 85

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PRIOR APPLICATION NUMBER: JP97/346686  
 PRIOR FILING DATE: 1997-12-16  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Patent Ver. 2.0  
 SEQ ID NO: 4  
 LENGTH: 894  
 TYPE: DNA  
 ORGANISM: Bacillus stearothermophilus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(894)  
 US-09-367-528A-4  
 Alignment Scores:  
 Pred. No.: 134e-70  
 Score: 650.00  
 Percent Similarity: 67.78%  
 Best Local Similarity: 49.63%  
 Query Match: 44.74%  
 Matches: 134  
 Conservative: 49  
 Mismatches: 85  
 Indels: 2  
 Gaps: 1  
 US-09-925-637-64 (1-287) x US-09-367-528A-4 (1-894)  
 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25  
 28 CTCACGAGCAAAACAGCGCGTGAACAGCGCTCTCCGTTATATAGCGCCTTAGAA 87  
 26 MetAspThrGlnLeuGluGluSerMetLeuTyrSerLeuAsnAlaGlyIlyValGlyIle 45  
 88 GGGCCGCGCGAGCAAAAGCGGATGCGCTACTGATGAGCGCGCGCAACGAAATC 147  
 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluIlyValGlyIle 65  
 148 CGTCGCTGCTGCTTCTGTCACCGTTCGGCGCTGCGCAAAACCGCGCTCGAATG 207  
 66 LysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspAspLeuPro 85  
 208 CCGCGCGCGCGCGATGAATGATCAATGCTCTTGTATGATGATGATTTGCGG 267  
 86 AlaMetAspAspAspAspTyrArgArgGlyIlyLeuThrAsnHisLysValIlyGlyIlu 105  
 268 AGCATGACAAACATATTTGCGCGCGCGCAACCGCAACGAAATGATGCGCGAG 327  
 106 TrpThrAlaIleLeuAlaGluAspAlaLeuLeuThrIlyValAlaPheGluLeuIleSer 124  
 328 GCGATGCGCATCTTGGCGGCGGAGCGGCTGTATACGACCGCTTCAATTTGATCACCAG 387  
 125 SerAspAspArgLeuThrAspGluValIleValIleValLeuGlnArgLeuSerIle 143  
 388 ATGACAGATGAGCGCATCCCTCTCCGTCGCGCTTCATGCAACGCGTGGGAGAA 447  
 144 AlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSerGluIlyGln 163  
 448 GCGGCGCGTCCGAGAGGATGTGTCGCGCGAGCAGCATATGAGAGGAGGAGGAGAA 507  
 164 ProIleAspLeuGluThrLeuGluMetIleHisLysThrIlyThrGlyAlaLeuLeuThr 183  
 508 AGCGTACCGCTTCGAGCTCGAATCATTCATGCAATCAACCGGAGAAATGCTGCAA 567  
 184 PheAlaValMetSerIleAlaAspIleAlaAsnValAspAspThrThrLysGluIleVal 203  
 568 TACAGCGTGCAGCGCGCGCTTGTATGCGGCGCGTATGCCGCAACGCGGAGCTT 627  
 204 GluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuAspCys 223  
 628 GACGAATTCGCGCGCATGAGCTTGTCAATTCGATATTCGATATTCGATATTC 687  
 224 TyrGlyAspGluAlaLysLeuGlyIlyValGlySerAspLeuGluAsnLysSer 243  
 688 GAGGCGCGCAAAACAGCGCGCGTGTGAGCGAGCAACAAAGCAACAAAGCG 747  
 244 ThrIlyValSerLeuLeuGlyIlyAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263

DB 748 AGTATCCAGCGTGTGCTGCGCGCGCGGAGAGAAAGTGGCGTTCCATATCGAG 807  
 QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273  
 DB 808 GCGGCGCGAGCGCGCATTTACGAAACCGCGAC 837  
 RESULT 12  
 US-08-534-910B-1  
 Sequence 1, Application US/08534910B  
 Patent No. 5766911  
 GENERAL INFORMATION:  
 APPLICANT: KOIKE, Ayumi  
 APPLICANT: OBARA, Shusei  
 APPLICANT: NISHINO, Tokuzo  
 APPLICANT: OHNUMA, Shinichi  
 APPLICANT: NAKAZAWA, Takeshi  
 APPLICANT: OGURA, Kyoza  
 APPLICANT: KOYAMA, Tanetoshi  
 TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable  
 TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kenyon & Kenyon  
 STREET: 1025 Connecticut Avenue, N.W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.  
 ZIP: 20036-5405  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.25" Floppy Disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
 SOFTWARE: IBM/Word Perfect 6.1 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/534,910B  
 FILING DATE: 28-SEPT-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-25253  
 FILING DATE: 14-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Toffenetli, Judith L.  
 REGISTRATION NUMBER: 39,048  
 REFERENCE/DOCKET NUMBER: 77670/398  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)429-0796  
 TELEFAX: (202)429-1776  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 894 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus stearothermophilus  
 US-08-534-910B-1  
 Alignment Scores:  
 Pred. No.: 5.52e-70  
 Score: 645.00  
 Percent Similarity: 68.63%  
 Best Local Similarity: 47.97%  
 Query Match: 44.39%  
 Matches: 130  
 Conservative: 56  
 Mismatches: 79  
 Indels: 6  
 Gaps: 2  
 US-09-925-637-64 (1-287) x US-08-534-910B-1 (1-894)  
 1 MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAla 20  
 DB 1 ATGCGCGAGCTTTCATGACAGTTTCTCAACAGCGAGCAAAACAGCGCGTGAACAGCG 60  
 QY 21 IleAsnLysSerValMet-----AspThrGlnLeuGluGluSerMetLeuTyr 36







APPLICANT: Gwynn, Michael  
 TITLE OF INVENTION: 1spA  
 FILE REFERENCE: GM10205  
 CURRENT APPLICATION NUMBER: US/09/275,742  
 CURRENT FILING DATE: 1999-03-24  
 NUMBER OF SEQ ID NOS: 2  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO: 1  
 LENGTH: 876  
 TYPE: DNA  
 ORGANISM: Streptococcus pneumoniae  
 US-09-275-742-1

Alignment Scores:  
 Pred. No.: 1,93e-58 Length: 876  
 Score: 551.00 Matches: 122  
 Percent Similarity: 64.89% Conservative: 48  
 Best Local Similarity: 46.56% Mismatches: 88  
 Query Match: 37.92% Indels: 4  
 Gaps: 3

US-09-925-637-64 (1-287) x US-09-275-742-1 (1-876)

28 ThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAlaGlyGlyLysArgIleArgPro 47  
 73 TCTAGTTACGGAGGAGTCTGTTCTCTATTCTATTCATGCTGGTGCAGAGCTATTCGGCT 132  
 48 ValLeuLeuLeuLeuThrLeuAspSerLeuAsn--ThrGluTyrGluLeuGlyMetLys 66  
 133 TTTCTCTTTGTTAAAGTTCTGGAAGCTTGAGCTTGATCCATCAAACTGCTCAAGCCGAC 192  
 67 SerAlaIleAlaLeuGlnMetIleHisThrTyrSerLeuIleHisAspAspLeuProAla 86  
 193 GTAGCTACTGCTCTGGAGATGATTCATACAGGAGCTTGATTCACGATGACCTTCCTGCT 252  
 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGluTyr 106  
 253 ATGATGATGATGATGATTCAGAGAGGCGGTAAACCATCAAGAAATTCGGTGAAGCT 312  
 107 ThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSerAsp 126  
 313 ATGGCCATTTTGGCTGAGATGCTTCTTATTCAGACCCATGAGCTTGATTCGGTGAAGCA 372  
 127 AspArgLeuThrAspGluValLysIleValLeuGlnArgLeuSerIleAlaSerGly 146  
 373 GAT--TTGCCAAGTCAATCAAGTGGCTTGATTCCTCAACTATCTGCTTCAGGT 429  
 147 HisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGlnProIleAsp 166  
 430 AGCTGGGATATGGTGGAGGCAAGTTTGGATATGAGAGGCGCAACACGACACTTGTCT 489  
 167 LeuGlnThrLeuGlnMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaVal 186  
 490 CTGGAAGAACTTCACTATTCATGCAATTAAGCTGGAAGTTACTAGCCCTATCCCTTC 549  
 187 MetSerAlaIleAlaSerIleAlaAsnValAspAspThrThrLysGluHisLeuGlnSerTyr 206  
 550 CAAGCGGACGCTTATATAGCTGAATGTCACTGAAATGAGGTGAAGCTGAAACCTGTG 609  
 207 SerTyrHisLeuGlnMetMetPheGlnIleLysAspAspLeuLeuAspCysTyrGlyAsp 226  
 610 CGTGAATGATTTGACTGCTTTTCAAGTCAAGATATATGATGATGAGAGGCTAGT 669  
 227 GluAlaLysLeuGlnLysLysValGlySerAspLeuGlnLysAsnLysSerThrTyrVal 246  
 670 TTGAGGAATTCGGCAAGACCTCAAAAGATCTGCAAGACAGAAATCAACTATCTCT 729  
 247 SerLeuLeuGlnLysAspGlyAlaGluAspLysLeuThrTyrHisLysArgAlaAlaVal 266  
 730 GGCCTGTGGGCTTGGAAAGATCATTTGTTGTAACCAAACTGAGTCAAGCTAAT 789  
 267 AspGluLeuThrGlnIleAspGluGln-----PheAsnThrLysHisLeuLeuGluIle 284

DB 790 GATAAATTAGAGAAATTTGCCAGAGCTTCCTTTGAACAGAAATGATTGTAAGTGA 849  
 QY 285 ValAsp 286  
 DB 850 GTAGAA 855

RESULT 15  
 US-08-961-527-76/c

Sequence 76, Application US/08961527  
 Patent No. 6420135  
 GENERAL INFORMATION:  
 APPLICANT: Charles Kunsch  
 TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 391  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/961,527

FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PB340P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 76:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10011 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear

US-08-961-527-76

Alignment Scores:  
 Pred. No.: 1.3e-56 Length: 10011  
 Score: 549.00 Matches: 121  
 Percent Similarity: 65.27% Conservative: 50  
 Best Local Similarity: 46.18% Mismatches: 87  
 Query Match: 37.78% Indels: 4  
 Gaps: 3

US-09-925-637-64 (1-287) x US-08-961-527-76 (1-10011)

28 ThrGlnLeuGlnGlnSerMetLeuTyrSerLeuAsnAlaGlyGlyLysArgIleArgPro 47  
 7806 TCTAGTTACGGAGGAGTCTGTTCTCTATTCTATTCATGCTGGTGCAGAGCTATTCGGCT 7747  
 48 ValLeuLeuLeuLeuThrLeuAspSerLeuAsn--ThrGluTyrGluLeuGlyMetLys 66  
 7746 TTTCTCTGTTTGAAGTTCTGGAAGCTTGCAAGTTTACCATCAAACTGCTCAAGCGCAG 7687  
 67 SerAlaIleAlaLeuGlnMetIleHisThrTyrSerLeuIleHisAspAspLeuProAla 86  
 7686 GTAGCTACTGCTCTGAGATGATTCATACAGGAGCTTGATTCACGATACCTTCCTGCT 7627  
 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlyGluTyr 106  
 7626 ATGATGATGATGATTCATTCAGAGAGGCGGTAAACCATCAAGAAATTCGGTGAAGCT 7567



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 30, 2003, 05:44:03 ; Search time 341 Seconds  
(without alignments)  
2772.950 Million cell updates/sec

Title: US-09-925-637-64  
Perfect score: 1453  
Sequence: 1 MTNLPMNKLIDEVNNELSA.....ELTQIDQFNTKLLIIVDL 287

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues  
Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO.epool/US09925637/rnatc.26112003\_153613\_19096/app\_query.fasta\_1.455  
-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rmpb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bases -START=1 -END=1 -MATRIX=blonsum62  
-TRANS=human40.csi -LIST=45 -DOCCALIGN=200 -THR SCORE=100 -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09925637@cgn2\_1\_221@rnatc.26112003\_153613\_19096  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:\*

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3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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17:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result: Query Match Length DB ID Description  
No. Score  
1 1453 100.0 861 10 US-09-925-637-63 Sequence 63, Appl

2	1453	100.0	861	14	US-10-084-205-63	Sequence 63, Appl
3	1453	100.0	1893	8	US-08-781-986A-155	Sequence 155, App
4	1442	99.2	882	9	US-09-815-242-8485	Sequence 8485, Ap
5	1415	97.4	864	9	US-09-815-242-4184	Sequence 4184, Ap
6	690	47.5	413	9	US-09-815-242-2822	Sequence 2822, Ap
7	635	43.7	811	10	US-09-974-300-1015	Sequence 1015, Ap
8	596	41.0	882	9	US-09-815-242-6533	Sequence 6533, Ap
9	587.5	40.4	758	10	US-09-070-927A-55	Sequence 55, Appl
10	570	39.2	337	9	US-09-815-242-3275	Sequence 3275, Ap
11	549	37.8	876	9	US-09-815-242-9499	Sequence 9499, Ap
12	547	37.6	876	9	US-09-815-242-9175	Sequence 9175, Ap
13	516.5	35.5	891	10	US-09-934-903-13	Sequence 934, Appl
14	516.5	35.5	891	10	US-09-934-868-71	Sequence 71, Appl
15	516.5	35.5	891	11	US-09-941-947A-19	Sequence 19, Appl
16	504.5	34.7	1470	13	US-10-108-915-25	Sequence 25, Appl
17	497.5	34.2	888	9	US-09-815-242-7142	Sequence 7142, Ap
18	497.5	34.2	1830121	14	US-10-329-960-1	Sequence 1, Appl
19	494.5	34.0	1441	13	US-10-108-915-21	Sequence 21, Appl
20	487.5	33.6	1268	13	US-10-108-915-17	Sequence 17, Appl
21	485.5	33.4	900	9	US-09-815-242-5972	Sequence 5972, Ap
22	485.5	33.4	900	12	US-10-006-909-11	Sequence 11, Appl
23	485.5	33.4	5963	12	US-10-006-909-13	Sequence 13, Appl
24	474.5	32.7	888	9	US-09-815-242-7873	Sequence 7873, Ap
25	473	32.6	900	9	US-09-815-242-9986	Sequence 9986, Ap
26	467	32.1	1612	12	US-10-166-225A-157	Sequence 157, App
27	465.5	32.0	1131	12	US-09-934-778-1	Sequence 1, Appl
28	438	30.1	1087	12	US-10-349-508-15	Sequence 15, Appl
29	380.5	26.2	1062	13	US-10-108-915-15	Sequence 15, Appl
30	376.5	25.9	912	11	US-09-941-947A-25	Sequence 25, Appl
31	376.5	25.9	912	12	US-10-218-118-1	Sequence 1, Appl
32	375	25.8	640681	10	US-09-790-988-1	Sequence 1, Appl
33	373.5	25.7	912	9	US-09-815-242-7285	Sequence 7285, Ap
34	372.5	25.6	912	9	US-09-815-242-7450	Sequence 7450, Ap
35	356	24.5	973	13	US-10-108-915-13	Sequence 13, Appl
36	352	24.2	536165	11	US-09-939-964-1	Sequence 1, Appl
37	332	22.8	951	14	US-10-166-037-3	Sequence 3, Appl
38	328	22.6	498	10	US-09-974-300-5453	Sequence 5453, Ap
39	328	22.6	973	13	US-10-108-915-11	Sequence 11, Appl
40	326	22.4	1128	14	US-10-156-761-140	Sequence 140, Ap
41	326	22.4	9025608	14	US-10-156-761-1	Sequence 1, Appl
42	321	21.7	498	10	US-09-974-300-5438	Sequence 5438, Ap
43	315.5	21.1	888	12	US-10-166-225A-184	Sequence 184, App
44	311.5	21.4	969	9	US-09-815-242-8505	Sequence 8505, Ap
45	311.5	21.4	1161	13	US-10-108-915-37	Sequence 37, Appl

# ALIGNMENTS

RESULT 1  
US-09-925-637-63  
Sequence 63, Application US/09925637  
Patent No. US2002010338A1  
GENERAL INFORMATION:  
APPLICANT: Chai  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: PB560  
CURRENT APPLICATION NUMBER: US/09/925, 637  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/151, 933  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781, 986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956, 171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009, 861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 63  
LENGTH: 861  
TYPE: DNA



Db 601 GAACATTGAAAGTATAGTATCATTTAGTATGATGTTCCAGATTAAGAATGATTTA 660  
Qy 221 LeuaspCyserThyTyrValSerLeuGluAlaValLeuGluValSerValGlySerAspLeuGluAsn 240  
Db 661 TTAGACTGCTATGATGATGAAGCAAAAGTAAAGTAAAGTGGGCGACGATCTTGAAAT 720  
Qy 241 AsnLysSerThyTyrValSerLeuGluValAspGluValAspLeuValSerLeuThyTyr 260  
Db 721 AATTAAGTACGTACGTACGTATTTATTTAGGAAAGATGCGCCAGAGATTAATTGACTTAT 780  
Qy 261 HisArgAspAlaAlaValAspGluLeuThrGlnLeuAspGluGlnPheAsnThrLysHis 280  
Db 781 CATAGAGACGACAGCAGGATGAACCTAACCAATTGATGACATTCATACAAAACAC 840  
Qy 281 LeuLeuGlnLysValAspLeu 287  
Db 841 TTATTAGAAATCGTTGATTTA 861

RESULT 3  
US-08-781-986A-155/c  
Sequence 155, Application US/08781986A  
Publication No. US2003054436A1  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781, 986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 155:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1893 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-155

Alignment Scores:  
Pred. No.: 8.55e-163 Length: 1893  
Score: 1453.00 Matches: 287  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-09-925-637-64 (1-287) x US-08-781-986A-155 (1-1893)  
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Db 1314 ATGACCAATCATCCGATGATTAATTAATGATGAAGTCAATTAATGATTAATTCGCTGGC 1255  
Qy 21 LeuAsnLysSerValMetAspThrGlnLeuGluGlnSerMetLeuLysSerLeuAsnAla 40  
Db 1254 AATTAATAATCAGTAAATGATGATCTGCTAGAAAGAAATGATGTTGATTCATTAATAATGCT 1195  
Qy 41 GlyLysArgLysArgProValLeuLeuLeuLeuThyLeuAspSerLeuAsnThrGlu 60  
Db 1194 GAGGTAAACGATCCGACGACATTCCTGTTATTAATCACTTAATTCATCAATAATACCGAG 1135  
Qy 61 TyrGlnLeuGlyMetLysSerAlaLeuAlaGlnMetLysThrLysSerLeuLeu 80  
Db 1134 TATGATTTAGTATGATGAAGCCCAATTCAGTAAATGATTCATCATATTCATCACTTAT 1075  
Qy 81 HisAspAspLeuProAlaMetAspAsnAspPyrArgArgGlyLysLeuThrAsnHis 100  
Db 1074 CATGATGACCTACACAGATGATTAATGATGATTAATGACGAGAAATTAACAAATTCAT 1015  
Qy 101 LysValTyrGlyGluThrPheAlaLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120  
Db 1014 AATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955  
Qy 121 GluLeuLysSerSerAspAspArgLeuThrAspGluValLysLysValLeuGlnArg 140  
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Qy 141 LeuSerLysLysSerGlyHisValGlyMetValGlyGlnMetLeuAspMetGlnSer 160  
Db 894 CTTGCAATGACAAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835  
Qy 161 GlnGlyGlnProLysAspLeuGlnThrLeuGlnMetLysLysThrLysThrGlyAla 180  
Db 834 GAAAGCCCAACAAATGATCTTGAATCTTGAATGATCAACAAACAAACAAACGAGACA 775  
Qy 181 LeuLeuThrPheAlaValMetSerAlaAlaAspLysAlaAsnValAspAspThrLys 200  
Db 774 TTATTACTTTTGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715  
Qy 201 GlnHisLeuGlnSerLysSerLysThrHisLeuGlyMetMetPheGlnLysAspAspLeu 220  
Db 714 GAACATTTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655  
Qy 221 LeuAspCyserThyTyrValSerLeuGluAlaValSerLeuGlyLysValGlySerSerLeuGluAsn 240  
Db 654 TTAGACTGCTATGATGATGAACAAAGTAAAGTAAAGTGGGCGACGATCTTGAAAT 595  
Qy 241 AsnLysSerThyTyrValSerLeuGluLysAspGlyValGluAspLeuValSerLeuThyTyr 260  
Db 594 AATTAAGTACGTACGTACGTATTTATTTAGGAAAGATGCGCCAGAGATTAATTGACTTAT 535  
Qy 261 HisArgAspAlaAlaValAspGluLeuThrGlnLeuAspGluGlnPheAsnThrLysHis 280  
Db 534 CATAGAGACGACAGCAGTGTGATGAACCTAACCAATTGATGACATTCATACAAAACAC 475  
Qy 281 LeuLeuGlnLysValAspLeu 287  
Db 474 TTATTAGAAATCGTTGATTTA 454

RESULT 4  
US-09-815-242-8485  
Sequence 8485, Application US/09815242  
Patent No. US2002061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

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1 // FILE REFERENCE: ELITRA.011A
2 // CURRENT APPLICATION NUMBER: US/09/815,242
3 // CURRENT FILING DATE: 2001-03-21
4 // PRIOR APPLICATION NUMBER: 60/191,078
5 // PRIOR FILING DATE: 2000-03-21
6 // PRIOR APPLICATION NUMBER: 60/206,848
7 // PRIOR FILING DATE: 2000-05-23
8 // PRIOR APPLICATION NUMBER: 60/207,727
9 // PRIOR FILING DATE: 2000-05-26
10 // PRIOR APPLICATION NUMBER: 60/242,578
11 // PRIOR FILING DATE: 2000-10-23
12 // PRIOR APPLICATION NUMBER: 60/253,625
13 // PRIOR FILING DATE: 2000-11-27
14 // PRIOR APPLICATION NUMBER: 60/257,931
15 // PRIOR FILING DATE: 2000-12-22
16 // PRIOR APPLICATION NUMBER: 60/269,308
17 // PRIOR FILING DATE: 2001-02-16
18 // NUMBER OF SEQ ID NOS: 14110
19 // SOFTWARE: FastSeq for Windows 4.0
20 // SEQ ID NO 8485
21 // LENGTH: 882
22 // TYPE: DNA
23 // ORGANISM: Staphylococcus aureus
24 // FEATURE:
25 // NAME/KEY: CDS
26 // LOCATION: (1)...(882)
27 // US-09-815-242-8485

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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1015
LENGTH: 811
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1015

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Pred. No.: 6,85e-66 Length: 811
Score: 635.00 Matches: 125
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Best Local Similarity: 52.52% Mismatches: 62
Query Match: 43.70% Indels: 2
DB: 10 Gaps: 1

US-09-925-637-64 (1-287) x US-09-974-300-1015 (1-811)
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Qy 50 LeuLeuLeuThrLeuAspSerLeuAsnThrGlyTyGluLeuGlyMetLysSerAlaIle 69
Db 157 GTTTCGCCCTTCTTCATGCTACGCAAGAAAGCAAGACCGCAATTCAGTCGATGC 216
Qy 70 AlaLeuGluMetIleHisThrTySerLeuIleHisAspAspLeuProAlaMetAspAsn 89
Db 217 GCGGTGAATGATCCATACGATATTCATTAATCATGACGACCTCCCTGTATGATGAC 276
Qy 90 AspAspTyrrArgArgGlyLyLeuLeuThrAsnHisLysValTyrglyGluTTPThAlaIle 109
Db 277 GATGACCTCGAAGAGGTAAAGCCGACAAACCAAAATTAACGGGGAGCGACCGCAT 336
Qy 110 LeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSerAsp-----Asp 127
Db 337 CTCGCGGAGAGCGCTTATTAACCGAAAGCTTCAAAATGATCATCTTCATATGCTTCT 396
Qy 128 ArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIleAlaSerGlyHis 147
Db 397 GATGTATCCGCTGAAAAGCGCATCAGACTGTAACGAGCTGATTCGGCAGCGGGGCC 456
Qy 148 ValGlyMetValGlyGlyGlnMetLeuAspMetLysSerGlyGlnProIleAspLeu 167
Db 457 GAAGGCAATGCGCGGCTGATTTGATATGAAACCGGATCAAAAGTCGTATCTCTT 516
Qy 168 GluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaValMet 187
Db 517 GATGAACCTGACGCAATCCACGAAAGAAAAGCGCTAACTCTTCAGCTTCAGGCTCAT 576
Qy 188 SerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeuGluSerTySer 207
Db 577 GCGGAGACCATTTCTGACATGATCGAATAAAGATCGAAAGCTGCGGAGTAATCAGC 636
Qy 208 TyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuLeuAspCySTyrglyAspGlu 227
Db 637 CATCATATCGGACATCGCTTCACATCAGATACATCTTTTGACCTTGAAAGCTCGAG 696
Qy 228 AlaLysLeuGlyLysLysValGlySerAspLeuGluLysAsnLysSerThrTyrrValSer 247
Db 697 GATGAAGTCGCAAAAGGATCGGATCGGACCTTCAACGAAAGGATGACGATTCCTCG 756
Qy 248 LeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrrHisArgAspAlaAla 265

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Db 757 CTCCTTCGCTGAGCGCGCCAGCAAAAACCTGATGATGATATTTGAAAAAGCA 810
RESULT 8
US-09-815-242-6533
Sequence 6533, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6533
LENGTH: 882
TYPE: DNA
ORGANISM: Enterococcus faecalis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(882)
US-09-815-242-6533

Alignment Scores:
Pred. No.: 3.43e-61 Length: 882
Score: 596.00 Matches: 134
Percent Similarity: 65.29% Conservative: 56
Best Local Similarity: 46.05% Mismatches: 91
Query Match: 41.02% Indels: 10
DB: 9 Gaps: 5

US-09-925-637-64 (1-287) x US-09-815-242-6533 (1-882)
Qy 1 MetThrAsnLeuProMetAsn-----LysLeuIleAspGluValAsnAsnGluLeuSer 18
Db 1 ATACGAAATTTTGTCACACGCACTTACCGCTTGTTGAAAAAATCATGTCGATTTT--- 57
Qy 19 ValAlaIleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTyrrSer 38
Db 58 -----ATCGACAATATATCTGAATAATGAGCGTTTGAAAGAACAAATGCTCATCTCA 111
Qy 39 AsnAlaGlyGlyLySarGlieArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsn 58
Db 112 CACGACGCTGCAAAAGATTAACCCCGCTATTGCTCTAACCAACAGTGGCGGCTTTTCAA 171
Qy 59 ThrGluTyrgluLeu---GlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrr 77
Db 172 AAAGAGATGAAACGCAAGACTATCAATGAGTGGCTGCTTTTAAAGATGATTCATACGAT 231
Qy 78 SerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrrArgArgGlyLysLeu 97

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Qy 218 AspAspLeuLeuAspCysTrgIyAspGluAlaIyLeuGlyIySlyValIglYserAsp 237
|||
Db 7290 GAGGACTTATTATGACCAAGTACGAGATTAGTAAAGTAAAGCCGAGAT 7349
|||
Qy 238 LeuGluAsnAsnIySerTrgIyValSerLeuLeuGlyIyAspGlyValIglYAspIyS 257
|||
Db 7350 GAAGCCTTGTAATAAAGTACGATCCAGCTTCTAGGATTCGCGGAAAGATGCG 7409
|||
Qy 258 LeuThrTyr 260
|||
Db 7410 CTAAACAT 7418
|||

RESULT 10
US-09-815-242-3275/C
; Sequence 3275, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3275
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-3275

Alignment Scores:
Pred. No.: 1,04e-58 Length: 337
Score: 570.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 39.23% Indels: 0
Gaps: 0

US-09-925-637-64 (1-287) x US-09-815-242-3275 (1-337)

Qy 76 ThrTyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGly 95
|||
Db 336 ACATATTCATCTTATTCATGATGACCTACCGCATGATATATGATTTTCACGCGGA 277
|||

Qy 96 LysLeuThrAsnHisIySlyValIyTrgIyGluTrpThrAlaIleLeuAlaGlyAspAlaLeu 115
|||
Db 276 AAATTAAACAATCAATAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 217
|||

Qy 116 LeuThrLysAlaIleGluLeuIleSerSerAspAspArgLeuThrAspGluValIySlyIle 135
|||
Db 216 TTAACTAAAGCATTTGAATCTTATTCAGTGAATGATGATTAATCTGATGAAGTAAATAATA 157
|||
```

```
Qy 136 ValLeuLeuGluIleArgLeuSerIleAlaSerGlyHisValIglYMetValIglYIleMet 155
|||
Db 156 AAAGTTCTACACAGCGCTGCTCAATACGAAAGTGCATCTTGGAATGATGATGATGATGATGAT 97
|||
Qy 156 LeuAspMetGlnSerIleGluGlnProIleAspLeuGluThrLeuGluMetIleHisIyS 175
|||
Db 96 TTGATATGCAAAAGCAAGGCCCAACCAATGATCTTGAAACTTGGAAATGATACACAAA 37
|||

Qy 176 ThrLysThrGlyAlaLeuLeuThrPheAlaValMet 187
|||
Db 36 ACAAAAACAGAGCATATTATTAACCTTTGCGGTTATG 1
|||

RESULT 11
US-09-815-242-9499
; Sequence 9499, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9499
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(876)
US-09-815-242-9499

Alignment Scores:
Pred. No.: 1,35e-55 Length: 876
Score: 549.00 Matches: 121
Percent Similarity: 65.27% Conservative: 50
Best Local Similarity: 46.18% Mismatches: 87
Query Match: 37.78% Indels: 4
Gaps: 3

US-09-925-637-64 (1-287) x US-09-815-242-9499 (1-876)

Qy 28 ThrGluLeuLeuGluSerMetLeuTyrSerLeuAsnAlaGlyIySlyArgIleArgPro 47
|||
Db 73 TCTAGTTTACGGAGAGCTGTTCTCTATTCATTCATGCTGATGCGCAAGCATATTCGGCT 132
|||

Qy 48 ValLeuLeuLeuLeuThrLeuAspSerLeuAsn--ThrGluTyrGluLeuGlyMetLys 66
|||
Db 133 TTCTCTTGTAGAACTTCTGAAAGCCTTGCAAGTTACATCAAACTGCTCAGCGCAG 192
|||
```

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QY 67 SerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspLeuProAla 86
DB 193 GTAGCTACTGCTTGGAGATGATTCATACAGGAGCTTGATTCACATGACCTTCCTGCT 252
QY 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisIleValTyrGlyGluTyr 106
DB 253 ATGAGATGATGACATTCATTCAGAGAGGCGGTAAACCAATCAAGAAATTCGGTGAAGCT 312
QY 107 ThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaIleHisGluLeuIleSerSerAsp 126
DB 313 ATGGCCATTTTGGCTGAGATGAGCTTATCTTACACCAATATGCTTGATTCGCGCAGCA 372
QY 127 AspArgLeuThrAspGluValIleLysIleValLeuGluIleArgLeuSerIleAlaSerGly 146
DB 373 GAT---TTGCCAAGTCAGATTAAGTGAGCTTATTCCTCACTTCCTTCCTTCAGGT 429
QY 147 HisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGlnProIleAsp 166
DB 430 AGCTGGGTATGGTGGCAGGCAAGTTTGATATGAGAGGCGCAACACGACACTGTCT 489
QY 167 LeuGluThrLeuGluMetIleHisIleLysThrLysThrGlyAlaLeuLeuThrPheAlaVal 186
DB 490 TTGGAAAGAACTTCAGATTATTCATGCCAATTAAGACTGGGAAGTTACTAGCTATCCCTTC 549
QY 187 MetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisIleGluIleSerTyr 206
DB 550 CAAGCGGACGACTTTATAGCTGATTCATCTGCAATTCAGGAAAGCTGAAAGCTGAG 609
QY 207 SerTyrHisLeuGluGlyMetMetPheGlnIleLysAspAspLeuAspCysTyrGlyAsp 226
DB 610 GGTGAATTGATGATGACTTCCTTTCAGAGTCAAGATGATGATGATGATGATGATGATGAT 659
QY 227 GluAlaLysLeuGluGlyLysLysValGlySerAspLeuGluAsnLysSerThrTyrVal 246
DB 670 TTGAGAAATTCGCGCAAGACACTCAAAAGATCTGCGCAGAGCAAAATCAACTATCCCT 729
QY 247 SerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAspAlaAlaVal 266
DB 730 GCCCTTTGGGCTTGGAGAGATTCATTCCTTTGTAACCAACCTCGGATCAAGCTAAT 789
QY 267 AspGluLeuThrGlnIleAspGluGln-----PheAsnThrLysHisIleLeuGluIle 284
DB 790 GAAAAATTTGAAGAAATTCGCCACAGGCTTCCTTGAAGACAGATGATGATGATGATGAT 849
QY 285 ValAsp 286
DB 850 GTAGAA 855

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## RESULT 12

```

US-09-815-242-9175
Sequence 9175, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26

```

```

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9175
LENGTH: 876
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(876)
US-09-815-242-9175
Alignment Scores:
Pred. No.: 2,339-55 Length: 876
Score: 547.00 Matches: 120
Percent Similarity: 64.89% Conservative: 50
Best Local Similarity: 45.80% Mismatches: 88
Query Match: 37.65% Indels: 4
DB: 9 Gaps: 3
US-09-925-637-64 (1-287) x US-09-815-242-9175 (1-876)
QY 28 ThrGluLeuGluGluSerMetLeuTyrSerLeuAsnAlaGlyLysArgIleArgPro 47
DB 73 TCTAGTTACGGGAGGCTCTTCTCTATTCATTCATGCTGAGTGGCAAGCTATTCGGCT 112
QY 48 ValLeuLeuLeuLeuThrLysAspSerLeuAsnThrGluTyrGlu---LeuGlyMetLys 66
DB 133 TTCTCTGTTGTAAGATTCGTAAGCTTCGACAGCTTCATCAACCTGCTCAGCGCAG 192
QY 67 SerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspLeuProAla 86
DB 193 GTAGCTACTGCTTGGAGATGATTCATACAGGAGCTTGATTCACATGACCTTCCTGCT 252
QY 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisIleValTyrGlyGluTyr 106
DB 253 ATGAGATGATGACATTCATTCAGAGAGGCGGTAAACCAATCAAGAAATTCGGTGAAGCT 312
QY 107 ThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaIleHisGluLeuIleSerSerAsp 126
DB 313 ATGGCCATTTTGGCTGAGATGAGCTTATCTTACACCAATATGCTTGATTCGCGCAGCA 372
QY 127 AspArgLeuThrAspGluValIleLysIleValLeuGluIleArgLeuSerIleAlaSerGly 146
DB 373 GAT---TTGCCAAGTCAGATTAAGTGAGCTTATTCCTCACTTCCTTCCTTCAGGT 429
QY 147 HisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGlnProIleAsp 166
DB 430 AGCTGGGTATGGTGGCAGGCAAGTTTGATATGAGAGGCGCAACACGACACTGTCT 489
QY 167 LeuGluThrLeuGluMetIleHisIleLysThrLysThrGlyAlaLeuLeuThrPheAlaVal 186
DB 490 TTGGAAAGAACTTCAGATTATTCATGCCAATTAAGACTGGGAAGTTACTAGCTATCCCTTC 549
QY 187 MetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisIleGluIleSerTyr 206
DB 550 CAAGCGGACGACTTTATAGCTGATTCATCTGCAATTCAGGAAAGCTGAAAGCTGAG 609
QY 207 SerTyrHisLeuGluGlyMetMetPheGlnIleLysAspAspLeuAspCysTyrGlyAsp 226
DB 610 GGTGAATTGATGATGACTTCCTTTCAGAGTCAAGATGATGATGATGATGATGATGATGAT 659
QY 227 GluAlaLysLeuGluGlyLysLysValGlySerAspLeuGluAsnLysSerThrTyrVal 246
DB 670 TTGAGAAATTCGTAAGACACTCAAAAGATCTGCGCAGAGCAAAATCAACTATCCCT 729

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Oy      247 SerLeuLeuGLyLyAspLyAlaGLyAspLyLeuThrThiSarGAspAlaAlaVal 266
Db      730 GCCTTGCTGGCGCTTGGAAGAGTCGATCGCTTTGTGAACCAACCTCGATCAAGCTAAT 789
Oy      267 AspGluLeuThrGluIleAspGluGln-----PheAsnThrLyshiSLeuLeuGluIle 284
Db      790 GAAAAATTGGAAGAATAATTCCGACGAGCTTCCTTTGAAACAGAAATCGATTGTAAGTGA 849
Oy      285 ValAsp 286
Db      850 GTAGAA 855

RESULT 13
US-09-934-903-13
; Sequence 13, Application US/09934903
; Patent No. US20020102690A1
; GENERAL INFORMATION:
; APPLICANT: Kofias, Matheos
; APPLICANT: Odum, J. Martin
; APPLICANT: Schenzle, Andreas J.
; APPLICANT: No. US20020102690A1ton, Kelley C.
; APPLICANT: Tombl, Jean-Francois
; APPLICANT: Rouviere, Pierre
; APPLICANT: Picataggio, Stephen
; APPLICANT: Cheng, Diong
; TITLE OR INVENTION: Genes Involved in Isoprenoid Compounds Production
; FILE REFERENCE: CL1646 US NA
; CURRENT APPLICATION NUMBER: US/09/934, 903
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229, 907
; PRIOR FILING DATE: September 1, 2001
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Methylobionas 16a
; FEATURE:
; OTHER INFORMATION: ORF7
US-09-934-903-13

Alignment Scores:
Pred. No.: 1,03e-51 Length: 891
Score: 516.50 Matches: 113
Percent Similarity: 63.75% Conservative: 47
Best Local Similarity: 45.02% Mismatches: 88
Query Match: 35.55% Indels: 3
DB: 10 Gaps: 2

US-09-925-637-64 (1-287) x US-09-934-903-13 (1-891)
Oy      23  LySserValMetAspThrGlnLeuGluGlnSerMetLeuTyrSerLeuAsnAlaGlyGly 42
Db      76  GAAACATATCAGCCACAACAACCTTGATTCAGGCGCATGCGCTATTCCTGATTGAACGGCGGG 135
Oy      43  LySarGluIleArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGlu 62
Db      136  AAACGCCACCGCGCCCTTGTTGCTTATTCGACCGCGGTGACGCTTGGCGCTTGCACGAAAC 195
Oy      63  LeuGluMetCysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAsp 82
Db      196  GTGCTGATGCGCCGCGCTTGCGCGGTGAGAAATTCATCATGTGATTGCTGATTCACGAC 255
Oy      83  AspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLyLeuLeuThrAsnHisIstysVal 102
Db      256  GATCGCGCGCGCATGACACAGATATCTGCGCCGCGCGGAAACCGACCTGTCAAGGCT 315
Oy      103  TyrGlyGluTyrTPThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLySAlaPheGluLeu 122
Db      316  TACGACGAGGCCACCGCATTTTGGCGCGGCGACGCACTCAAGCGCTGGCGCTTGAAGTT 375
Oy      123  IleSerSerAspAspArgLeuThrAspGlu-----ValLyAlaIleYsValLeuGlnArg 140

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Db	376	CTGGCCAAAGACCCCGGCATCAACCGTCAGTCCCGGCTCGCTGAAATGATACAGGCT	43			
Qy	141	LeuSer1Leu1Aser1Yhi1Sva1Gly1MetVal1Gly1Ygl1MetLeu1AspMetGlnSer	167			
Db	436	TTGACCCGGCCGACCGGCTCTCAAGGACATGCTGGGGCGGTCAAGCCATGATCTGGCTCC	495			
Qy	161	GIuGI1Ygl1Pro1Leu1Asp1Leu1Glu1Thr1Leu1Glu1Met1Leu1Sly1Thr1Yse1Thr1Gly1Ala	180			
Db	496	GTCGGCCCGCAAAATTGACGCTGCCCGGAATCTCGAATAATGATATTCACAAAGCTGGCGCC	555			
Qy	181	LeuLeuThr1Phe1AlaVal1---MetSer1Ala1Asp1Leu1Ala1AsnVal1Asp1Asp1Thr1Thr	195			
Db	556	CTGATCCGGGCGACGCGTCAATCTGGGGGATATTCAAACCGCATCTGATATCTTGGCTC	615			
Qy	200	LYeGI1His1Leu1Glu1Ser1Yse1Ytr1His1Leu1Gly1Met1Met1Phe1Gln1His1Leu1Asp1Asp	215			
Db	616	GCCAAAGAACTGGATCTACTATCTCAATGACATAGCGCTGTGTCTTCAGGTCAAGGTCAAGACAC	675			
Qy	220	LeuLeuAsp1Cys1Trp1Gly1Asp1Glu1Ala1Yse1Glu1Yly1Sly1Val1Gly1Ser1Asp1Leu1Glu	235			
Db	676	ATTCTCGACATTCGAAGCCGACACCGGACACTCGGCAAGACTCAAGGCGCAAGACATCGAT	735			
Qy	240	Asn1Asn1Yse1Ser1Thr1Ytr1Val1Ser1Leu1Glu1Yly1Asp1Gly1Ala1Glu1Asp1Yly1Leu1Thr	255			
Db	736	AAGACAAACCCGACCTTACCTCGCTATTTGGGCATGCGTGGCGCAAAACAAAGGCCAG	795			
Qy	260	TYrHis1Arg1Asp1Ala1Ala1Val1Asp1Glu1Leu1Thr	270			
Db	796	GAATTGCACGAACAAAGACGCTCGAAAGCTTAAAG	828			
RESULT 14						
US-09-934-868-71	Sequence 71, Application US/09934868					
Patent No. US20020137190A1						
GENERAL INFORMATION:						
APPLICANT: Koffas, Matcheos						
APPLICANT: Odom, James M						
APPLICANT: Schenzle, Andreas J						
TITLE OF INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN						
FILE REFERENCE: CL1596 US NA						
CURRENT APPLICATION NUMBER: US/09/934,868						
CURRENT FILING DATE: 2001-08-22						
PRIOR APPLICATION NUMBER: 60/229,858						
PRIOR FILING DATE: 2000-09-01						
NUMBER OF SEQ ID NOS: 81						
SOFTWARE: Microsoft Office 97						
SEQ ID NO 71						
LENGTH: 891						
TYPE: DNA						
ORGANISM: Methylomonas 16a						
FEATURE:						
OTHER INFORMATION: ORF7 ISPA						
US-09-934-868-71						
Alignment Scores:						
Pred. No.:	1,03e-51	Length:	891			
Score:	516.50	Matches:	113			
Percent Similarity:	63.75%	Conservative:	47			
Best Local Similarity:	45.02%	Mismatches:	88			
Query Match:	35.55%	Indels:	3			
Db:	10	Gaps:	2			
US-09-925-637-64 (1-287) x US-09-934-868-71 (1-891)						
Qy	23	LYeSer1Val1Met1Asp1Thr1Glu1Glu1Glu1Ser1Met1Leu1Ytr1Ser1Leu1Asn1Ala1Gly1Y	42			
Db	76	GAATAATATCTCGCCACAAACCTTGATATCAGGCGCATCGCTATTCGATTTGAACGGCGGC	135			
Qy	43	LYsArg1Leu1Arg1Pro1Val1Leu1Leu1Leu1Thr1Leu1Asp1Ser1Leu1Asn1Thr1Glu1Ytr1Glu	62			
Db	136	AAACGACACCGGCGCTTGTGTGACTTATGACACCGGTACGCTTGGGCTTCCGGAAC	195			
Qy	63	LeuGly1Met1Yse1Ser1Ala1Leu1Glu1Met1Leu1His1Thr1Ytr1Ser1Leu1His1Asp	82			

```

Db      196 GTCCTGATGCGCGGCTTCGCGGAGTATTCATCATGATGATTCGATTCACGAC 255
Qy      83 AspleuProAlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisVal 102
Db      256 GATCTCGCGCCAGCAAGATGATCTCGCGCGCAACCGACCTGTCCAAAGGCT 315
Qy      103 TyGlyGlnPheThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGlnLeu 122
Db      316 TACGACAGAGCCACCGCATTTTGCGCGGACGCACTGACAGCGCGCTTGAAGTT 375
Qy      123 ILeSerSerAspAspArgLeuThrAspGln-----ValLysIleValLeuGlnArg 140
Db      376 CTGGCCACAGCACCCTGATCACCCTGATGCGCGCGCTGCGTGAATAATGATCAGGCT 435
Qy      141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
Db      436 TTGACCCGCGCCAGCGCTCTCAAGGCTGTGGCGGTCAAGCCATCGATCTCGGCTCC 495
Qy      161 GluGlyGlnProIleAspLeuGlnLeuThrLeuGlnMetIleHisLysThrLysThrGlyAla 180
Db      496 GTCCGCGCGCAATTCAGCTGCTCCGGAATCTGAAACATGCAATTCACAAAGACTGGCGCC 555
Qy      181 LeuLeuThrPheAlaVal--MetSerAlaIleAspIleAlaAsnValAspAspThrThr 199
Db      556 CTGATCCGCGCCAGCGCTCATCTGGCGGATTCATTCAAACCGCATCTGATCTTCGCTC 615
Qy      200 LysGlnHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAsp 219
Db      616 GCCAAGAACTGTGATCATATGCAATGCCAAATGATGCTGTTCGTTCCAGGTCAAAGCGAC 675
Qy      220 LeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysValGlySerAspLeuGln 239
Db      676 ATTCCTGACATTCAGAACCGCACCGGACACTGGGAGAGCTCAGGCGAAGCATCGAT 735
Qy      240 AsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGlnAspLysLeuThr 259
Db      736 AACGACAAACCGACCTACCTCGGCTATTGGCATGGCTGCCCAAAAGCCGACG 795
Qy      260 TyrHisArgAspAlaAlaValAspGlnLeuThr 270
Db      796 GAATTCACGAAACAGACATCGAAAGCTTAAACG 828

```

RESULT 15  
US-09-941-947A-19

```

; Sequence 19, Application US/09941947A
; Publication No. US20030003528A1
; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qiong
; APPLICANT: DiCosimo, Deana J.
; APPLICANT: Kofinas, Matheos
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odom, J. Martin
; APPLICANT: Picataggio, Steve
; APPLICANT: Rouviere, Pierre E.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CL1903 US NA
; CURRENT APPLICATION NUMBER: US/09/941,947A
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Methylobionas 16a
; US-09-941-947A-19

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Alignment Scores:

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Pred. No.: 1,03e-51 Length: 891
Score: 516.50 Matches: 113
Percent Similarity: 63.75% Conservative: 47
Best Local Similarity: 45.02% Mismatches: 88
Query Match: 35.55% Indels: 3
DB: 11 Gaps: 2

```

US-09-925-637-64 (1-287) x US-09-941-947A-19 (1-891)

```

Qy      23 LysSerValMetAspThrGlnLeuGlnGlySerMetLeuTyrSerLeuAlaGlyGly 42
Db      76 GAAATATCTGCGCACAACTTTCATCAGGCCATCGCTATTCCTATTGAAGCGCGC 135
Qy      43 LysArgIleArgProValLeuLeuLeuLeuLeuLeuAspSerLeuLeuThrGlyGln 62
Db      136 AAACGACCCCGCGCTTGTGACTTATGCGACCGGTGACGCTTGGCGTTCGCGAAGAC 195
Qy      63 LeuGlyMetLysSerAlaIleAlaLeuGlnMetIleHisThrTyrSerLeuIleHisAsp 82
Db      196 GTCCTGATGCGCGGCTTCGCGGAGTATTCATCATGATTCATTCGCTGATTCACGAC 255
Qy      83 AspleuProAlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisVal 102
Db      256 GATCTCGCGCCATGAGACAGATGATTCGCGCGCGCAACCGACCTGTCCAAAGGCT 315
Qy      103 TyGlyGlnPheThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGlnLeu 122
Db      316 TACGACAGAGCCACCGCATTTTGGCGCGGACGCACTCAGGCGCTTGTGAAGTT 375
Qy      123 ILeSerSerAspAspArgLeuThrAspGln-----ValLysIleValLeuGlnArg 140
Db      376 CTGGCCACAGCACCCTGCTACCTGCTGACGCGCGGCTGCGTGAATAATGATCAGGCT 435
Qy      141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
Db      436 TTAGCCCGCGCCAGCGCTCTCAAGGCTGTGGCGGTCAAGCCATCGATCTCGGCTC 495
Qy      161 GluGlyGlnProIleAspLeuGlnLeuThrLeuGlnMetIleHisLysThrLysThrGlyAla 180
Db      496 GTCCGCGCGCAATTCAGCTGCTCCGGAATCTGAAACATGCAATTCACAAAGACTGGCGCC 555
Qy      181 LeuLeuThrPheAlaVal--MetSerAlaIleAspIleAlaAsnValAspAspThrThr 199
Db      556 CTGATCCGCGCCAGCGCTCATCTGGCGGATTCATTCAAACCGCATCTGATCTTCGCTC 615
Qy      200 LysGlnHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAsp 219
Db      616 GCCAAGAACTGTGATCATATGCAATGCCAAATGATGCTGTTCGTTCCAGGTCAAAGCGAC 675
Qy      220 LeuLeuAspCysTyrGlyAspGlnAlaLysLeuGlyLysValGlySerAspLeuGln 239
Db      676 ATTCCTGACATTCAGAACCGCACCGGACACTGGGAGAGCTCAGGCGAAGCATCGAT 735
Qy      240 AsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGlnAspLysLeuThr 259
Db      736 AACGACAAACCGACCTACCTCGGCTATTGGCATGGCTGCCCAAAAGCCGACG 795
Qy      260 TyrHisArgAspAlaAlaValAspGlnLeuThr 270
Db      796 GAATTCACGAAACAGACATCGAAAGCTTAAACG 828

```

Search completed: November 30, 2003, 07:55:56  
Job time : 352 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:29:55 ; Search time 21 Seconds  
(without alignments)  
578.248 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 1453

Sequence: 1 MTNLPNNKLIIDEVNNELSA.....ELTQIDQENFKHLEIVDL 287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1436	98.8	293	3	US-09-276-873-2
2	1015	69.9	302	4	US-09-134-001C-3171
3	657	45.2	297	1	US-08-534-910B-9
4	654	45.0	297	3	US-08-886-466-2
5	654	45.0	297	3	US-09-475-304-2
6	654	45.0	297	4	US-09-101-126-3
7	653	44.9	297	1	US-08-534-910B-7
8	650	44.7	297	1	US-08-534-910B-8
9	650	44.7	297	4	US-08-534-910B-10
10	650	44.7	297	4	US-09-367-528A-5
11	646	44.5	297	4	US-09-367-528A-1
12	645	44.4	297	1	US-08-534-910B-6
13	644	44.3	297	4	US-09-367-528A-3
14	551	37.9	291	4	US-09-275-742-2
15	533	36.7	312	4	US-09-107-532A-6724
16	521	35.9	393	3	US-09-187-050-34
17	520.5	35.8	393	3	US-09-187-050-2
18	520.5	35.8	393	3	US-09-187-050-14
19	520.5	35.8	393	3	US-09-187-050-16
20	520.5	35.8	393	3	US-09-187-050-18
21	520.5	35.8	393	3	US-09-187-050-20
22	520.5	35.8	393	3	US-09-187-050-22
23	520.5	35.8	393	3	US-09-187-050-24
24	520.5	35.8	393	3	US-09-187-050-26
25	520.5	35.8	393	3	US-09-187-050-27
26	520.5	35.8	393	3	US-09-187-050-28
27	520.5	35.8	393	3	US-09-187-050-29

28	520.5	35.8	393	3	US-09-187-050-30	Sequence 30, Appl
29	520.5	35.8	393	3	US-09-187-050-31	Sequence 31, Appl
30	520.5	35.8	393	3	US-09-187-050-32	Sequence 32, Appl
31	520.5	35.8	393	3	US-09-187-050-33	Sequence 33, Appl
32	517	35.6	285	3	US-09-187-050-12	Sequence 12, Appl
33	480	33.0	280	4	US-09-634-238-303	Sequence 303, App
34	474.5	32.7	401	4	US-09-252-991A-26387	Sequence 26387, A
35	465.5	32.0	377	4	US-09-420-211-2	Sequence 2, Appl1
36	442	30.4	308	4	US-09-328-352-4190	Sequence 4190, Ap
37	376.5	25.9	302	1	US-07-783-705A-1	Sequence 1, Appl1
38	346	23.8	298	1	US-08-095-726-4	Sequence 4, Appl1
39	346	23.8	298	1	US-08-096-043-4	Sequence 4, Appl1
40	346	23.8	298	1	US-08-093-577-4	Sequence 4, Appl1
41	346	23.8	298	1	US-08-096-623A-4	Sequence 4, Appl1
42	346	23.8	307	1	US-08-095-726-2	Sequence 2, Appl1
43	346	23.8	307	1	US-08-096-043-2	Sequence 2, Appl1
44	346	23.8	307	1	US-08-093-577-2	Sequence 2, Appl1
45	346	23.8	307	1	US-08-096-623A-2	Sequence 2, Appl1

#### ALIGNMENTS

```
RESULT 1
; Sequence 2, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwina Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: Isopa
; FILE REFERENCE: GM10208
; CURRENT APPLICATION NUMBER: US/09/276, 873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-276-873-2

Query Match      98.8%; Score 1436; DB 3; Length 293;
Best Local Similarity 99.0%; Pred. No. 1.7e-132;
Matches 284; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIIDEVNNELSAVINKSVMDTQLEBSMLYSLNAGKRIRPVLLLTLDLSLNT 60
DB 1 MTNLPNNKLIIDEVNNELSAVINKSVMDTQLEBSMLYSLNAGKRIRPVLLLTLDLSLNT 60
QY 61 YELGKMSAIALEMIHITYSLIHDDLPMNDYDRGKLTNNKRYGWTAILAGDALLTKAF 120
DB 61 YELGKMSAIALEMIHITYSLIHDDLPMNDYDRGKLTNNKRYGWTAILAGDALLTKAF 120
QY 121 ELISSDRLTDEYKIKVLRSLASGVHVGWGMQMDQSEGPDILETLEMHTKRTGA 180
DB 121 ELISSDRLTDEYKIKVLRSLASGVHVGWGMQMDQSEGPDILETLEMHTKRTGA 180
QY 181 LITFAVMSADIANVDITTEKHEBSYSYHIGMFFQIKDDLDCYGDBAKKGKVGSDLEN 240
DB 181 LITFAVMSADIANVDITTEKHEBSYSYHIGMFFQIKDDLDCYGDBAKKGKVGSDLEN 240
QY 241 NKSTYVSLGKGADBDKLTTHRDAAVDELTOIDQENFKHLEIVDL 287
DB 241 NKSTYVSLGKGADBDKLTTHRDAAVDELTOIDQENFKHLEIVDL 287

RESULT 2
US-09-134-001C-3171
; Sequence 3171, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
```

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3171  
LENGTH: 302  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3171

Query Match 69.9%; Score 1015; DB 4; Length 302;  
Best Local Similarity 68.6%; Pred. No. 2,7e-91;  
Matches 197; Conservative 41; Mismatches 49; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIDEVNNELSVAINKSVMTQLEESMLYSINAGKRRIRPVLLLTLSINTE 60  
DB 10 MKKLQNNKLIININTSLINKSIQSSPLKTNLEESMKYSINAGKRRIRPVLLLTLSINTE 69  
QY 61 YELGMSKSAILEMHTSYLIHDDLPAAMDNDYRGRKLTNNKYYGEWTAIAGDALLTKAF 120  
DB 70 YQGLNSALALEMHTSYLIHDDLPAAMDNDYRGRKLTNNKYYGEWTAIAGDALLTKAF 129  
QY 121 ELISSDRLTDEVYKIKVLRSLASGHVGVGOMLDMOSEGQPIDLETLEMTHTKTA 180  
DB 130 ELVSNPTTIDSVYKSIKRLSKASGHLGVGQALDMESGKSIKLETLEMTHTKTA 189  
QY 181 LTRFAVMSADIANVDDTTEHLESYSHLGMMFOIKODLLDCYGEPAKKGKVSLEN 240  
DB 190 LNFESVAAADIVAQVEONIAKNLDEFSHLGMMFOIKODLLDYGSESKKGKVSIDIVN 249  
QY 241 NKSTYSILGKQGAEDKLTTHRDAVDELTDQDEQFTKHLLEIVDL 287  
DB 250 HKSTYSILGKQGAEDKLTTHRDAVDELTDQDEQFTKHLLEIVDL 296

RESULT 3  
US-08-534-910B-9  
Sequence 9, Application US/08534910B  
Patent No. 5766911  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Ayumi  
APPLICANT: OBATA, Shusei  
APPLICANT: NISHINO, Tokuzo  
APPLICANT: OHNUMA, Shinichi  
APPLICANT: NAKAZAWA, Takeshi  
APPLICANT: OGURA, Kyoza  
APPLICANT: KOYAMA, Tanetsoshi  
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable  
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Ther  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1025 Connecticut Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.  
ZIP: 20036-5405  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.25" Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: IBM/Word Perfect 6.1 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,910B  
FILING DATE: 28-SEPT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-25253  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Totenetti, Judith L.  
REGISTRATION NUMBER: 39,048  
REFERENCE/DOCKET NUMBER: 77670/398  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)429-1776  
TELEFAX: (202)429-0796  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 297 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
US-08-534-910B-9

Query Match 45.2%; Score 657; DB 1; Length 297;  
Best Local Similarity 47.7%; Pred. No. 2,7e-56;  
Matches 133; Conservative 57; Mismatches 83; Indels 6; Gaps 2;

QY 1 MTNLPNNKLIDEVNNELSVAINKSVMTQLEESMLYSINAGKRRIRPVLLLTLSINTE 56  
DB 1 MQLSVGEPLNEKQKAVETALSYIRLESGPAKTKKAMVSLGKRRIRPVLLLTSTVRA 60  
QY 57 LNTVELGMSKSAILEMHTSYLIHDDLPAAMDNDYRGRKLTNNKYYGEWTAIAGDALL 116  
DB 61 LGKDPVAGPVCAIMHTSHLHDDLPSMDNDLRKCKPTNHKVFGEWTAIAGDALL 120  
QY 117 TKAFELIS--SDRLTDEVYKIKVLRSLASGHVGVGOMLDMOSEGQPIDLETLEMT 174  
DB 121 TYAFQILTEIDBRIPSVRLRIETRLAVAGGAVQAADMESEKTLTSLSELYTH 180  
QY 175 KTKTGALLTFPAVMSADIANVDDTTEHLESYSHLGMMFOIKODLLDCYGEPAKKGK 234  
DB 181 RHKTGMGLQVSYHAGLLIGGADARQTRLEDEFAHHLGLFQIRDDITLDEGAEKIGKV 240  
QY 235 GSDLENKSTYSILGKQGAEDKLTTHRDAVDELTDQID 273  
DB 241 GSDPSNNKATYPALISLAGAKKELTFHIEAQRHLNAD 279

RESULT 4  
US-08-886-466-2  
Sequence 2, Application US/08886466C  
Patent No. 6040165  
GENERAL INFORMATION:  
APPLICANT: Narita, Keisshi  
APPLICANT: Ishida, Chiaki  
APPLICANT: Takeuchi, Yoshie  
APPLICANT: Onuma, Shinkichi  
APPLICANT: Nishino, Tokuzo  
TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE  
FILE REFERENCE: 77670/494  
CURRENT APPLICATION NUMBER: US/08/886,466C  
CURRENT FILING DATE: 1997-07-10  
EARLIER APPLICATION NUMBER: JP 8-191635  
EARLIER FILING DATE: 1996-07-03  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Bacillus stearothermophilus  
US-08-886-466-2

Query Match 45.0%; Score 654; DB 3; Length 297;  
Best Local Similarity 47.7%; Pred. No. 5,2e-56;  
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;







```

ADDRESSER: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-10

```

```

Query Match          44.7%; Score 650; DB 1; Length 297;
Best Local Similarity 47.3%; Pred. No. 1,3e-55;
Matches 132; Conservative 55; Mismatches 86; Indels 6; Gaps 2;

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```

QY 1 MNTLPNKLIDEVNNELSVAINKSV---DTGLEESMLYSINAGKRIIPVLLLTDS 56
DB 1 MQLSVEQFLNEOKOAVETALSRIERLEGPARKKAMAYSLEAGGRIRPILLSTVQA 60
QY 57 LNTVEYLGMKSAIALAMHHTYSLIHDDLPAMDNDYRGRGLTNHXYGEMTALLADALL 116
DB 61 LGGDPVAVGVPAACATEMHTYSLIHDDLPAMDNDYLRGKPTNHKVFGEAMAILAGDGLL 120
QY 117 TFAFELIS--SDRLTDEVKIKVLORLSIASGHVGVGGQMLDMOSEGQPIDLETLEM 174
DB 121 TYAFQILTEIDDRIRPSVRLRIERLAKAAGPEGVAVAGQADMEGEGKTLTSELEYIH 180
QY 175 KRTYGTALLTFVAVSAADIANVDTTKEHLESYSYHIGMMFOIKDILLDCYGEBAKIGKY 234
DB 181 RHHTGMALQSVAGALLIGADARQTRRELEDFAAHGLAFQIRDDIILDEGAEEKIGKPY 240
QY 235 GSDLENNKSTYVSLGKDGAEKLTYHRDAVDELTOID 273
DB 241 GSDQNNKATYTPALLSLAGAKELAFHTEAQRHLRNAD 279

```

```

RESULT 10
US-09-367-528A-5
Sequence 5, Application US/09367528A
Patent No. 6395525
GENERAL INFORMATION:
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA.
TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
FILE REFERENCE: PH-586
CURRENT APPLICATION NUMBER: US/09/367,528A
PRIOR FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: JP97/346686
PRIOR FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 6

```

```

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-367-528A-5

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```

Query Match          44.7%; Score 650; DB 4; Length 297;
Best Local Similarity 49.6%; Pred. No. 1,3e-55;
Matches 134; Conservative 49; Mismatches 85; Indels 2; Gaps 1;

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QY 6 MNKLIDEVNNELSVAINKSVMDTGLEESMLYSINAGKRIIPVLLLTDSINTEYELGM 65
DB 10 LNEQKQAVETALSRIERLEGPARKKAMAYSLEAGGRIRPILLSTVRLALGKDPVGL 69
QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRGRGLTNHXYGEMTALLADALLTFAFELIS- 124
DB 70 PVACATEMHTYSLIHDDLPAMDNDYLRGKPTNHKVFGEAMAILAGDGLTTFAPOLITE 129
QY 125 -SDRLTDEVKIKVLORLSIASGHVGVGGQMLDMOSEGQPIDLETLEMHTKRTGALLT 183
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAVAGQADMEGEGKTLTSELEYIHRKTKMLQ 189
QY 184 FAVMSAADIANVDTTKEHLESYSYHIGMMFOIKDILLDCYGEBAKIGKVGSDLENKNS 243
DB 190 YSVHAGALLIGADARQTRRELEDFAAHGLAFQIRDDIILDEGAEEKIGKPVSDQNNKA 249
QY 244 TVVSLGKDGAEKLTYHRDAVDELTOID 273
DB 250 TYPALLSLAGAKELAFHTEAQRHLRNAD 279

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RESULT 11
US-09-367-528A-1
Sequence 1, Application US/09367528A
Patent No. 6395525
GENERAL INFORMATION:
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
FILE REFERENCE: PH-586
CURRENT APPLICATION NUMBER: US/09/367,528A
PRIOR FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: JP97/346686
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
NAME/KEY: PEPTIDE
LOCATION: 82
OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,
OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, Trp, His or Pro.
US-09-367-528A-1

```

```

Query Match          44.5%; Score 646; DB 4; Length 297;
Best Local Similarity 49.3%; Pred. No. 3,2e-55;
Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;

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QY 6 MNKLIDEVNNELSVAINKSVMDTGLEESMLYSINAGKRIIPVLLLTDSINTEYELGM 65
DB 10 LNEQKQAVETALSRIERLEGPARKKAMAYSLEAGGRIRPILLSTVRLALGKDPVGL 69
QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRGRGLTNHXYGEMTALLADALLTFAFELIS- 124
DB 70 PVACATEMHTYSLIHDDLPAMDNDYLRGKPTNHKVFGEAMAILAGDGLTTFAPOLITE 129
QY 125 -SDRLTDEVKIKVLORLSIASGHVGVGGQMLDMOSEGQPIDLETLEMHTKRTGALLT 183
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAVAGQADMEGEGKTLTSELEYIHRKTKMLQ 189

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QY 184 FAVMSADIANVDDTTEHESYHIGMMFOIKODLLDCYGBEAKLGGKVGSDLENKS 243  
Db 190 YSVHAGALIGADARQTRREIDEPFAHLGLAFQIRDDILDIEGAEEKIGKVGSDQSNKA 249  
QY 244 TYVSLGKGABDKLTYHRDAVDELTOID 273  
Db 250 TYPALISLAGAKKELAFHIEAQRHLRNAD 279

## RESULT 12

US-08-534-910B-6  
; Sequence 6, Application US/08534910B  
; Patent No. 5766911  
; GENERAL INFORMATION:  
; APPLICANT: KOIKE, Ayumi  
; APPLICANT: OBATA, Shusei  
; APPLICANT: NISHINO, Tokuzo  
; APPLICANT: OHNIMA, Shinichi  
; APPLICANT: MAKIZAWA, Takeshi  
; APPLICANT: OGURA, Kyoza  
; APPLICANT: KOYAMA, Tanetoshi  
; TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable  
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Ther  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenyon & Kenyon  
; STREET: 1025 Connecticut Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: U.S.  
; ZIP: 20036-5405  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.25" Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
; SOFTWARE: IBM/Word Perfect 6.1 Windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/534, 910B  
; FILING DATE: 28-SEPT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-25253  
; FILING DATE: 14-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Toffenetti, Judith L.  
; REGISTRATION NUMBER: 39,048  
; REFERENCE/DOCKET NUMBER: 77670/398  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)428-1776  
; TELEFAX: (202)429-0796  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 297 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus stearothermophilus  
; US-08-534-910B-6

Query Match 44.4%; Score 645; DB 1; Length 297;  
Best Local Similarity 48.0%; Pred. No. 4e-55;  
Matches 130; Conservative 56; Mismatches 79; Indels 6; Gaps 2;

QY 1 MTNLPMNKLLIDVNNELSVAINKSVM---DTQLEBSMLYSINAGGKRIRPVLLLTDS 56  
Db 1 MAOLSVQFIFNEKQAVETLSRYIERLESPAKLKKAMAVSLGAGKRIRPILLSTVRA 60  
QY 57 LNTVEYLGMSAATALEMIHTSYSLIHDDLPAMNDNDYRGKLTNNKVVGEWTATIAAGDAL 116  
Db 61 LGKDPVAVGLPVACALIEHITHSLIHDDLPAMDNDLRGRGPTNNKVFGEEMALILAGDGL 120  
QY 117 TYAFELIS--SDRLTDEVKIKVLRSLASGVHVGGMMLDMOSEGQPIDLETLEMIH 174

Db 121 TYAFOLITEIDRRIPPSVRLIERLAKAAGEGVAGQAADEGKTLTISELEYIH 180  
QY 175 KTKTGALLTPAVMSADIANVDDTTEHESYHIGMMFOIKODLLDCYGBEAKLGGKV 234  
Db 181 RHKTGKQLQYSVAGALIGADARQTRREIDEPFAHLGLAFQIRDDILDIEGAEEKIGKPV 240  
QY 235 GSDLENKSTYVSLGKGABDKLTYHRDAA 265  
Db 241 GSDQSNKATYYPALLISLAGAKKELAFHIEA 271

## RESULT 13

US-09-367-528A-3  
; Sequence 3, Application US/09367528A  
; Patent No. 6395525  
; GENERAL INFORMATION:  
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA  
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene  
; FILE REFERENCE: PH-586  
; CURRENT APPLICATION NUMBER: US/09/367,528A  
; CURRENT FILING DATE: 1999-08-16  
; PRIOR APPLICATION NUMBER: JP97/346686  
; PRIOR FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Bacillus stearothermophilus  
; US-09-367-528A-3

Query Match 44.3%; Score 644; DB 4; Length 297;  
Best Local Similarity 49.3%; Pred. No. 5e-55;  
Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;

QY 6 MNKLIDEVNNELSVAINKSVMDTQLEBSMLYSINAGGKRIRPVLLLTDSINTERYELGM 65  
Db 10 LNEQKQAVETLSRYIERLESPAKLKKAMAVSLGAGKRIRPILLSTVRA LKDPVAVGL 69  
QY 66 KSAIALEMHTSYSLIHDDLPAMNDNDYRGKLTNNKVVGEWTATIAAGDALTYAFELIS- 124  
Db 70 PVACALIEHITHSLIHDDLPAMDNDLRGRGPTNNKVFGEEMALILAGDGLTYAFOLITE 129  
QY 125 -SDRLTDEVKIKVLRSLASGVHVGGMMLDMOSEGQPIDLETLEMIHKTGTGALLT 183  
Db 130 IDDERIPPSVRLIERLAKAAGEGVAGQAADEGKTLTISELEYIHRRKTGMLQ 189  
QY 184 FAVMSADIANVDDTTEHESYHIGMMFOIKODLLDCYGBEAKLGGKVGSDLENKS 243  
Db 190 YSVHAGALIGADARQTRREIDEPFAHLGLAFQIRDDILDIEGAEEKIGKVGSDQSNKA 249  
QY 244 TYVSLGKGABDKLTYHRDAVDELTOID 273  
Db 250 TYPALISLAGAKKELAFHIEAQRHLRNAD 279

## RESULT 14

US-09-275-742-2  
; Sequence 2, Application US/09275742  
; Patent No. 6130069  
; GENERAL INFORMATION:  
; APPLICANT: Wilding, Edwina Imogen  
; APPLICANT: Gwynn, Michael  
; TITLE OF INVENTION: ispa  
; FILE REFERENCE: GM10205  
; CURRENT APPLICATION NUMBER: US/09/275, 742  
; CURRENT FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 291  
; TYPE: PRT

ORGANISM: Streptococcus pneumoniae  
US-09-275-742-2

Query Match 37.9%; Score 551; DB 3; Length 291;  
Best Local Similarity 46.6%; Pred. No. 6e-46;  
Matches 122; Conservative 48; Mismatches 88; Indels 4; Gaps 3;

28 TQLEEMTSLNAGKRRIRPVLLLTLDLSLN-TEVELGMSATALEMHTYSLIHDDLPA 86  
25 SSAREVLSINHGKRRIRPVLLLTLEALQVITKRAHVAVALALEMHTYSLIHDDLPA 84  
87 MNDNDYRGRGLTNHXYGEMTALLAGDALLTKAFELISSDRLTDEVKIKVLRSLASG 146  
85 MDDDDYRGRGLTNHXYGEMTALLAGDALLTKAFELISSDRLTDEVKIKVLRSLASG 143  
147 HVMNAGQMLDMQSEGPIDLETLEMHTKTKGALLTFPVMASADIANVDTTKEHLEST 206  
144 SLGMVAGQVLDMEGHQHLSEBELQTHANKTKLAVPQAAAI1AELSPMQVXLKTV 203  
207 SYHAGMMFOIKDDLLDCYGEAKLGKVSDELNNKSTYVSLGKXGAEKDLTYHRDAV 266  
204 GELIGLAFQVRDVLVTASFEELGKTPQKQDAKSTYFALGLSEIAFCNQTLDQAN 263  
267 DELTQIDEQ--FNTKHLLEIVD 286  
264 DKLEIAQQLPFETESIVSVE 285

RESULT 15  
US-09-107-532A-6724

Sequence 6724, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSER: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION NUMBER: 60/085,598

APPLICATION DATA:

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6724:

SEQUENCE CHARACTERISTICS:

LENGTH: 312 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...312  
SEQUENCE DESCRIPTION: SEQ ID NO: 6724:  
US-09-107-532A-6724

Query Match 36.7%; Score 533; DB 4; Length 312;  
Best Local Similarity 44.5%; Pred. No. 3.8e-44;  
Matches 117; Conservative 48; Mismatches 96; Indels 2; Gaps 2;

13 VNNEISVALNKSVMDTQLESMLYSINAGKRRIRPVLLLTLDLSNTEVELGM-KSAIAL 71  
30 VEREILSFDEHTTDRGLYDAMSYSVAGGKRRIRPVLLLTAVASFPEDIDVPYQVAAAL 89  
72 EMHTYSLIHDLLPAMNDYRGRGLTNHXYGEMTALLAGDALLTKAFELISSDRLTD 131  
90 EMVHTYSLIHDLLPAMNDYRGRGLTNHXYGEMTALLAGDALLTKAFELISSDRLTD 148  
132 EVKIKVLRSLASGHHVGVGQMLDMQSEGPIDLETLEMHTKTKGALLTFPVMASAD 191  
149 SPRLILLQDLAVCAGSGQVAGQADIEGSKTSLSELAFTHERKTHLIRYALLAGI 208  
192 IANVDDTKEHLESYSLGMMFOIKDDLLDCYGEAKLGKVSDELNNKSTYVSLGK 251  
209 LAKQPEILILLQLAHEHLGLAFQIRDDLDVYGTTKTKGAKDERMEKNTYPRLLGL 268  
252 DGAEDKLTYHRDAVDELTOIDE 274  
269 EKTRALRIELLSANKIIDLEE 291

Search completed: November 26, 2003, 15:33:22  
Job time : 22 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 15:32:20 ; Search time 31 Seconds  
(Without alignments)  
1707.588 Million cell updates/sec

Title: US-09-925-637-64  
Perfect score: 1453  
Sequence: 1 MTNLPNKLIDEVNNELSYA.....ELTQDEQNTKHLITVDL 287

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues  
Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1453	100.0	287	10	US-09-925-637-64
2	1453	100.0	287	15	US-10-084-205-64
3	1442	99.2	293	9	US-09-815-242-12583
4	1415	97.4	288	9	US-09-815-242-5239
5	596	41.0	293	9	US-09-815-242-10630
6	549	37.8	291	9	US-09-815-242-13597
7	547	37.6	291	10	US-09-815-242-13273
8	516.5	35.5	297	10	US-09-934-903-14
9	516.5	35.5	297	11	US-09-934-868-72
10	516.5	35.5	297	11	US-09-941-947A-20
11	504.5	34.7	367	14	US-10-108-915-26
12	497.5	34.0	295	9	US-09-815-242-11239
13	494.5	34.0	350	14	US-10-108-915-22
14	487.5	33.6	369	14	US-10-108-915-18
15	485.5	33.4	299	9	US-09-815-242-10069

16	478.5	32.9	316	14	US-10-108-915-45	Sequence 45, Appl
17	474.5	32.7	295	9	US-09-815-242-11971	Sequence 11971, A
18	473	32.6	299	9	US-09-815-242-14084	Sequence 14084, A
19	467	32.1	287	12	US-10-166-225A-159	Sequence 159, App
20	465.5	32.0	377	10	US-09-934-778-2	Sequence 2, Appl1
21	402.5	27.7	316	14	US-10-108-915-16	Sequence 16, Appl1
22	402.5	27.7	316	14	US-10-108-915-20	Sequence 20, Appl1
23	376.5	25.9	303	11	US-09-941-947A-26	Sequence 26, Appl1
24	376.5	25.9	303	12	US-10-218-118-2	Sequence 2, Appl1
25	373.5	25.7	303	9	US-09-815-242-11382	Sequence 11382, A
26	372.5	25.6	303	9	US-09-815-242-11547	Sequence 11547, A
27	356	24.5	228	14	US-10-108-915-14	Sequence 14, Appl1
28	350	24.1	232	14	US-10-108-915-12	Sequence 12, Appl1
29	326	22.4	375	15	US-10-156-761-9190	Sequence 9190, App
30	315.5	21.7	296	12	US-10-166-225A-185	Sequence 185, App
31	311.5	21.4	322	9	US-09-815-242-12603	Sequence 12603, A
32	311.5	21.4	342	14	US-10-108-915-38	Sequence 38, Appl1
33	311.5	21.4	323	9	US-09-815-242-10321	Sequence 10321, A
34	311	21.4	344	15	US-10-156-761-8668	Sequence 8668, Ap
35	310	21.3	323	9	US-09-815-242-13734	Sequence 13734, A
36	309.5	21.3	295	10	US-09-547-267-1	Sequence 1, Appl1
37	309.5	21.3	295	11	US-09-920-923-2	Sequence 2, Appl1
38	308.5	21.2	312	9	US-09-815-242-5315	Sequence 5315, Ap
39	303	20.9	326	14	US-10-108-915-46	Sequence 46, Appl1
40	300.5	20.7	337	15	US-10-156-761-10534	Sequence 10534, A
41	300	20.6	293	11	US-09-920-923-37	Sequence 37, Appl1
42	294	20.2	329	11	US-09-815-242-11142	Sequence 11142, A
43	292	20.1	209	14	US-10-108-915-30	Sequence 30, Appl1
44	280	19.3	322	9	US-09-815-242-12031	Sequence 12031, A
45	269	18.5	342	14	US-10-108-915-34	Sequence 34, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-925-637-64  
Sequence 64, Application US/09925637  
Patent No. US2002010338A1  
GENERAL INFORMATION:  
APPLICANT: CNOI  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides  
FILE REFERENCE: PB560  
CURRENT APPLICATION NUMBER: US/09/925,637  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/23773  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/151,933  
PRIOR FILING DATE: 1999-09-01  
PRIOR APPLICATION NUMBER: US 08/781,986  
PRIOR FILING DATE: 1997-01-03  
PRIOR APPLICATION NUMBER: US 08/956,171  
PRIOR FILING DATE: 1997-10-20  
PRIOR APPLICATION NUMBER: US 60/009,861  
PRIOR FILING DATE: 1996-01-06  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 64  
LENGTH: 287  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-637-64  
Query Match 100.0%; Score 1453; DB 10; Length 287;  
Best Local Similarity 100.0%; Pred. No. 2.5e-139;  
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNKLIDEVNNELSYA.....ELTQDEQNTKHLITVDL 60  
DB 1 MTNLPNKLIDEVNNELSYA.....ELTQDEQNTKHLITVDL 60  
QY 61 YELGKSAIATLMTITVSLIHDLPAMDNDVDRGKLTNKKYGEWTAIADALTKAF 120

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Db 61 YELGMSAIALEMHTVSLIHDDLPMANDNDYRGRKLTNKKVYGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEVKIKVLRSLASGHVGVGGQMLDMOSEGQPIDETLEMIHKTGTGA 180
Db 121 ELISSDRLTDEVKIKVLRSLASGHVGVGGQMLDMOSEGQPIDETLEMIHKTGTGA 180
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
QY 241 NKSTTVSLGKDGAEDEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287
Db 241 NKSTTVSLGKDGAEDEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

RESULT 2
US-10-084-205-64
; Sequence 64, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB515P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 64
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-084-205-64

Query Match 100.0%; Score 1453; DB 15; Length 287;
Best Local Similarity 100.0%; Pred. No. 2,5e-139;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIDEVNNELSLVAINKSVMDTOLESMLYSINAGKRIRPVLLLTLDLSINTE 60
Db 1 MTNLPNNKLIDEVNNELSLVAINKSVMDTOLESMLYSINAGKRIRPVLLLTLDLSINTE 60
QY 61 YELGMSAIALEMHTVSLIHDDLPMANDNDYRGRKLTNKKVYGEWTAIIAGDALLTKAF 120
Db 61 YELGMSAIALEMHTVSLIHDDLPMANDNDYRGRKLTNKKVYGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEVKIKVLRSLASGHVGVGGQMLDMOSEGQPIDETLEMIHKTGTGA 180
Db 121 ELISSDRLTDEVKIKVLRSLASGHVGVGGQMLDMOSEGQPIDETLEMIHKTGTGA 180
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
QY 241 NKSTTVSLGKDGAEDEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287
Db 241 NKSTTVSLGKDGAEDEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

RESULT 3
US-09-815-242-12583
; Sequence 12583, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
```

```
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12583
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12583

Query Match 99.2%; Score 1442; DB 9; Length 293;
Best Local Similarity 99.3%; Pred. No. 3.4e-138;
Matches 285; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTNLPNNKLIDEVNNELSLVAINKSVMDTOLESMLYSINAGKRIRPVLLLTLDLSINTE 60
Db 1 MTNLPNNKLIDEVNNELSLVAINKSVMDTOLESMLYSINAGKRIRPVLLLTLDLSINTE 60
QY 61 YELGMSAIALEMHTVSLIHDDLPMANDNDYRGRKLTNKKVYGEWTAIIAGDALLTKAF 120
Db 61 YELGMSAIALEMHTVSLIHDDLPMANDNDYRGRKLTNKKVYGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEVKIKVLRSLASGHVGVGGQMLDMOSEGQPIDETLEMIHKTGTGA 180
Db 121 ELISSDRLTDEVKIKVLRSLASGHVGVGGQMLDMOSEGQPIDETLEMIHKTGTGA 180
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
QY 241 NKSTTVSLGKDGAEDEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287
Db 241 NKSTTVSLGKDGAEDEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

RESULT 4
US-09-815-242-5239
; Sequence 5239, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
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;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 5239  
;; LENGTH: 288  
;; TYPE: PRT  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-5239

Query Match 97.4%; Score 1415; DB 9; Length 288;  
Best Local Similarity 99.3%; Pred. No. 1,8e-135;  
Matches 280; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MNKLIDEVNNELSVAINKSVMDTOLESMLYSINAGKRIKRPVLLLTLDLSLNTVEYELGM 60  
QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLTKAFELISS 125  
DB 61 KSAIALEMHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLTKAFELISS 120  
QY 126 DRLTBEVKIKVLRSLIASGHVGMVGGQMLDMQSEQPIDLTLEMIHKTGALLTFA 185  
DB 121 DRLTBEVKIKVLRSLIASGHVGMVGGQMLDMQSEQPIDLTLEMIHKTGALLTFA 180  
QY 186 VNSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGKVGSDLENNKSTY 245  
DB 181 VNSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGKVGSDLENNKSTY 240  
QY 246 VSLGKGAEDKLTYHRDAVDELTOIDEOFTKHLLEIVDL 287  
DB 241 VSLGKGAEDKLTYHRDAVDELTOIDEOFTKHLLEIVDL 282

RESULT 5  
US-09-815-242-10630  
; Sequence 10630, Application US/09815242  
; Patent No. US2002061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA 011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625

;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 10630  
;; LENGTH: 293  
;; TYPE: PRT  
;; ORGANISM: Enterococcus faecalis  
US-09-815-242-10630

Query Match 41.0%; Score 596; DB 9; Length 293;  
Best Local Similarity 46.0%; Pred. No. 3.4e-52;  
Matches 134; Conservative 56; Mismatches 91; Indels 10; Gaps 5;

QY 1 MTNLPNN--KLIDEVNNELSVAINKSVMDTOLESMLYSINAGKRIKRPVLLLTLDLSIN 58  
DB 1 MTNLPNN--KLIDEVNNELSVAINKSVMDTOLESMLYSINAGKRIKRPVLLLTLDLSIN 57  
QY 59 TEYEL-GMSAIALEMHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLT 117  
DB 58 KEMETQDYVAASLEMIHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLT 117  
QY 118 KAFELISSDRLTDEVKIKVLRSLIASGHVGMVGGQMLDMQSEQPIDLTLEMIHKTG 177  
DB 118 KAFELISSDRLTDEVKIKVLRSLIASGHVGMVGGQMLDMQSEQPIDLTLEMIHKTG 176  
QY 178 TGAULTFAVMSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGKVGSD 237  
DB 177 TGAULTFAVMSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGKVGSD 236  
QY 238 LENNSTYSLGKGAEDKLTY--HRDAVDELTOIDEOFTKHLLEIV 285  
DB 237 LENNSTYSLGKGAEDKLTY--HRDAVDELTOIDEOFTKHLLEIV 287

RESULT 6  
US-09-815-242-13597  
; Sequence 13597, Application US/09815242  
; Patent No. US2002061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA 011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13597

```
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13597

Query Match      37.8%; Score 549; DB 9; Length 291;
Best Local Similarity 46.2%; Pred. No. 2e-47;
Matches 121; Conservative 50; Mismatches 87; Indels 4; Gaps 3;

QY 28 TOLEESWLYSLNAGKRIIPVLLLTLDLSLNTYEY-LGKMSALALEMHTYSLIHDDLP 86
DB 25 SSLRESVLYSIHAGKRIIPVLLLEVEALQVATIKPAHQAVALALEMHTYSLIHDDLP 84
QY 87 MDDNDYRGRKLTNNKKGEMWTAIAGDALITKAFELISSDRDLTDEKIKVLRSLASG 146
DB 85 MDDDDYRGRKLTNNKKGEMWTAIAGDALITKAFELISSDRDLTDEKIKVLRSLASG 143
QY 147 HGVWGQMLDMOEGOPIDLETLEMHTKTKGALLTFVMSAADIANVDTTKEHLESY 206
DB 144 SLGVVAGQVLDMEGEHQLSLBELQTIHANKTKGLAVPQAAAIILSPENQVTKTV 203
QY 207 SYHGMFQIKDILDCYGEBAKLGKVGSDLENKSTYVSLGKGAEDKLTYHRDAV 266
DB 204 GELIGLAFQVRDVLDTASFEEIGTKPQKDLQAEKSTYVSLGKGAEDKLTYHRDAV 263
QY 267 DELTOIDQ--FNTKHLLEIVD 286
DB 264 EKLEIAQVLPFETESIVSVE 285

RESULT 7
US-09-815-242-13273
; Sequence 13273; Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13273
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13273

Query Match      37.6%; Score 547; DB 9; Length 291;
Best Local Similarity 45.8%; Pred. No. 3.2e-47;
Matches 120; Conservative 50; Mismatches 88; Indels 4; Gaps 3;
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```
QY 28 TOLEESWLYSLNAGKRIIPVLLLTLDLSLNTYEY-LGKMSALALEMHTYSLIHDDLP 86
DB 25 SSLRESVLYSIHAGKRIIPVLLLEVEALQVATIKPAHQAVALALEMHTYSLIHDDLP 84
QY 87 MDDNDYRGRKLTNNKKGEMWTAIAGDALITKAFELISSDRDLTDEKIKVLRSLASG 146
DB 85 MDDDDYRGRKLTNNKKGEMWTAIAGDALITKAFELISSDRDLTDEKIKVLRSLASG 143
QY 147 HGVWGQMLDMOEGOPIDLETLEMHTKTKGALLTFVMSAADIANVDTTKEHLESY 206
DB 144 SLGVVAGQVLDMEGEHQLSLBELQTIHANKTKGLAVPQAAAIILSPENQVTKTV 203
QY 207 SYHGMFQIKDILDCYGEBAKLGKVGSDLENKSTYVSLGKGAEDKLTYHRDAV 266
DB 204 GELIGLAFQVRDVLDTASFEEIGTKPQKDLQAEKSTYVSLGKGAEDKLTYHRDAV 263
QY 267 DELTOIDQ--FNTKHLLEIVD 286
DB 264 EKLEIAQVLPFETESIVSVE 285

RESULT 8
US-09-934-903-14
; Sequence 14; Application US/09934903
; Patent No. US20020102690A1
; GENERAL INFORMATION:
; APPLICANT: Kotlaas, Mattheos
; APPLICANT: Odum, J. Martin
; APPLICANT: Schenzle, Andreas J.
; APPLICANT: No. US20020102690A1ton, Kelley C.
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Rouviere, Pierre
; APPLICANT: Piccataggio, Stephen
; APPLICANT: Cheng, Qiong
; TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
; FILE REFERENCE: C11646 US NA
; CURRENT APPLICATION NUMBER: US/09/934,903
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: September 1, 2001
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Methylobionas 16a
; FEATURE:
; OTHER INFORMATION: Amino acid sequences encoded by ORF7
US-09-934-903-14

Query Match      35.5%; Score 516.5; DB 10; Length 297;
Best Local Similarity 45.0%; Pred. No. 4.2e-44;
Matches 113; Conservative 47; Mismatches 88; Indels 3; Gaps 2;

QY 23 KSYMVTOLESWLYSLNAGKRIIPVLLLTLDLSLNTYEYELGKMSALALEMHTYSLIH 82
DB 26 ENILPOTLHOAMKYSVLANGGKRIIPVLLTATGQALGPENVLDAACAAVEFIHVSILHD 85
QY 83 DLPAKNDYRGRKLTNNKKGEMWTAIAGDALITKAFELISSDRDLTDE--VKIKVLR 140
DB 86 DLPAKNDYRGRKLTNNKKGEMWTAIAGDALITKAFELISSDRDLTDE--VKIKVLR 145
QY 141 LSTASGHWGQMLDMOEGOPIDLETLEMHTKTKGALLTFVMSAADIANVDTTKEHLESY 206
DB 146 LTRASGQGWGQALIDLSGVGRKLTPELENMHTKTKGALLTFVMSAADIANVDTTKEHLESY 205
QY 200 KEHLESYHLMGPMFQIKDILDCYGEBAKLGKVGSDLENKSTYVSLGKGAEDKLT 259
DB 206 AKKLDHYACTIGTSFQVKKDILDEADVTGLTGQKQKIDNDKPTYPALGMAKQKQAO 265
QY 260 YHRDAVDEL 270
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QY 191 DIANVDDTTKEHLESYSYHLGMMFOIKDLDLCYGBEAKLGGKVVGSDDLNNKSTYVSLG 250  
DQ 266 ILGGTDDVEYKLRKFRARYIGLLFQVVDLIDVTKSSQELGKTAKGDLVADKTYPRLLG 325  
QY 251 KQGAEDKLTTHRDAAVDELTOID 273  
DQ 326 IEKSKVFAAKLNKADQDLVGF 348

## RESULT 12

US-09-815-242-11239  
Sequence 11239, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyckind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,991  
PRIOR FILING DATE: 2000-12-32  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11239  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Haemophilus influenzae  
US-09-815-242-11239

Query Match 34.2%; Score 497.5; DB 9; Length 295;  
Best Local Similarity 41.0%; Pred. No. 3.5e-42;  
Matches 116; Conservative 52; Mismatches 100; Indels 15; Gaps 4;

QY 16 ELASVANKSVMDTLE-----ESMYSLNAGSKRIRPVLLLTLDLSLNTVEYELGM 65  
DQ 10 QVQTRIR-FLAQFEGIESHNAPLLEAMKRYALLGGKVRPFLVATGMLGKXQTL 68  
QY 66 KSAIALEMITYSLIHDDLPAMNDYRKGKLTNNKYYGWTAILAGDALLTAFAELISS 125  
DQ 69 YAAALIAIAHAYSLIHDDLPAMDDNLRGHPCHIOFDEATIALADALQSFAFELITK 128  
QY 126 DDLRLDVEKTKVLRSLASGNGVGMGLDMQSEOPIDLETLEMHHKTKGALLTFA 185  
DQ 129 TPNISTQKALIQILAQAGVQGMCLGQSLDLISHKQSLSELELHNNKTKGALL-IA 187  
QY 186 VMSAADIAN--VDDTTKEHLESYSYHLGMMFOIKDLDLCYGBEAKLGGKVVGSDDLNNK 242  
DQ 188 ALKAGFCSHFTDKREGLSLQYAAEIGLAFQVQDILIDIEGSAEIGQVAGADLDL 247  
QY 243 STYVSLIGKQGAEDKLTTHRDAAVDELTOIDEGNTTHLEIV 285  
DQ 248 STYPKLLIGLGAKQKADLVYASLSLEKIPDTTYALAEFI 290

## RESULT 13

US-10-108-915-22  
Sequence 22, Application US/10108915  
Publication No. US20020177204A1  
GENERAL INFORMATION:  
APPLICANT: Cahoon, Rebecca E.  
APPLICANT: Shen, Jennie  
APPLICANT: Williams, Mark  
TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases  
FILE REFERENCE: B81286 US NA  
CURRENT APPLICATION NUMBER: US/10/108,915  
CURRENT FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 22  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-108-915-22

Query Match 34.0%; Score 494.5; DB 14; Length 350;  
Best Local Similarity 43.3%; Pred. No. 9.2e-42;  
Matches 114; Conservative 42; Mismatches 98; Indels 9; Gaps 3;

QY 20 AINKSVMDT-----QLESMLYSINAGSKRIRPVLLLTLDLSLNTVEYELGKSAIALE 72  
DQ 69 AVNKGDDSVSLNEPKKIHAMRYSLAGSKRVRPVLCAACGLVGHGKATAPACALE 128  
QY 73 MHTTSLIHDDLPAMNDYRKGKLTNNKYYGWTAILAGDALLTAFAELISSDDRLTDS 132  
DQ 129 MHTTSLIHDDLPAMNDYRKGKLTNNKYYGWTAILAGDALLTAFAELISSDDRLTDS 188  
QY 133 VKI-KYLORSLASGNGVGMGLDMQSEG-OPIDLETLEMHHKTKGALLTFAVMSAA 190  
DQ 189 PRLRAIGELARSIGSEGLVAGVVDINSBGLADGLERLEFTHHKTALLLEGAVVLGA 248  
QY 191 DIANVDDTTKEHLESYSYHLGMMFOIKDLDLCYGBEAKLGGKVVGSDDLNNKSTYVSLG 250  
DQ 249 ILGGTDDVEYKLRKFRARYIGLLFQVVDLIDVTKSSQELGKTAKGDLVADKTYPRLLG 308  
QY 251 KQGAEDKLTTHRDAAVDELTOID 273  
DQ 309 IEKSKVFAAKLNKADQDLVGF 348

## RESULT 14

US-10-108-915-18  
Sequence 18, Application US/10108915  
Publication No. US20020177204A1  
GENERAL INFORMATION:  
APPLICANT: Cahoon, Rebecca E.  
APPLICANT: Shen, Jennie  
APPLICANT: Williams, Mark  
TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases  
FILE REFERENCE: B81286 US NA  
CURRENT APPLICATION NUMBER: US/10/108,915  
CURRENT FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 18  
LENGTH: 369  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-108-915-18

Query Match 33.6%; Score 487.5; DB 14; Length 369;  
Best Local Similarity 44.9%; Pred. No. 5,1e-41;  
Matches 111; Conservative 43; Mismatches 88; Indels 5; Gaps 4;

QY 13 VNNELVAINKSVMDT-QLEESMLYSINAGKRIKRPVLLLTLDLSINTEYELGKMSAIAL 71  
DB VNNALDAAL--ALRDPKRIHQAMRYSILLAGKRVPLCIACELVGTETATNIPAAAV 146  
QY 72 EMHTHTSLIHHDDLPAANDNDYRRGKLTNNKRVGEMTALLAGDALITKAF-LISSDRLL 130  
DB 147 EMHTHTSLIHHDDLPCMDNDLDRGKPTNNKRVGEDVAVLADLALFAPFVHAASTEGVS 206  
QY 131 DEKIKLQRLSLASGHVGMVGGOMLDMOSEG-QPIDLETLLEMIHKTGTGALLTFVMSA 189  
DB 207 PSRVVAIGLASITGEGVLAQVVDIDSEGVANGETLETFTHAKTALLLEAAVVG 266  
QY 190 ADIANVDDTTKEHLESYSYHLGMMFOIKDDLDLCYGBEAKLGRKVSDELENNKSTYVSL 249  
DB 267 AIVGGSDSEVEKLRKFRARCIGLLFQVVDILDTSSSEELGTAGKDLVADKVTYPKLL 326  
QY 250 GKGDAED 256  
DB 327 GIDKSKE 333

RESULT 15  
US-09-815-242-10069  
; Sequence 10069, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10069  
; LENGTH: 299  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-815-242-10069

Query Match 33.4%; Score 485.5; DB 9; Length 299;  
Best Local Similarity 41.8%; Pred. No. 6e-41;  
Matches 118; Conservative 42; Mismatches 117; Indels 5; Gaps 4;

QY 10 IDEVNNELVAINK-SYMDTQLESMLYSINAGKRIKRPVLLLTLDLSINTEYELGKMSA 68  
DB 11 VKQANQALSRFLAPLPQNTPVVETWQYALLGSKRLRPLVATGMFGVSTNTLDAPA 70

QY 69 IALEMHTHTSLIHHDDLPAANDNDYRRGKLTNNKRVGEMTALLAGDALITKAFELISSDD- 127  
DB 71 AAVECHIAVSLIHHDDLPAANDDDLRGKLTCHVKREBAALILAGDALQTLAPSLSDADM 130  
QY 128 -RLTDEVKIKVLQRLSLASGHVGMVGGOMLDMOSEGQPIDLETLLEMIHKTGTGALLTFV 186  
DB 131 PEVSDRDRISMISELASAGIAGMCGQALDIDABGKHVPLDALERIHHKTGALLIRAAV 190  
QY 187 -MSADIANVDDTTKEHLESYSYHLGMMFOIKDDLDLCYGBEAKLGRKVSDELENNKSTY 245  
DB 191 RLGALSAGDKGRRALPVLDKVAESIGLAFQVDDILDVVDATLTKRGQADQDLGKSTY 250  
QY 246 VSLGKGDAEDKLTYYRDAAVDELQIDEO-FNTKTLLEIVD 286  
DB 251 PALLGLEQARKKARLDLIDAROSLQJLABOSIDTSALMALAD 292

Search completed: November 26, 2003, 15:37:47  
Job time : 31 secs

